

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:31:51 ; Search time 1963.49 seconds  
(Without alignments)  
373.024 Million cell updates/sec

Title: US-09-927-267-13  
Perfect score: 35  
Sequence: 1 catgctagaatgagatgggctcactctgacct 35

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 1046368293 residues

Total number of hits satisfying chosen parameters: 843946

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_ph:\*  
7: gb\_pl:\*  
8: gb\_pl:\*  
9: gb\_pl:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
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1	18.6	53.1	77	11	G33119	G33119 Ey7976L Hu
2	17.6	50.3	51	6	AX157589	AX157589 Sequence
3	17.6	50.3	51	6	AX157591	AX157591 Sequence
4	17.2	49.1	38	6	ARI20506	ARI20506 Sequence
5	17.2	49.1	75	9	HS444350	AJ344350 Homo sapi
6	17.2	49.1	88	9	HS444350	AJ344350 Homo sapi
7	17.2	49.1	100	9	HS444350	AJ344350 Homo sapi
8	16.8	48.0	42	6	AR035931	AR035931 Sequence
9	16.8	48.0	42	6	AR035931	AR035931 Sequence
10	16.8	48.0	42	6	AR035931	AR035931 Sequence
11	16.6	47.4	38	6	AX343247	AX343247 Sequence
12	16.6	47.4	38	6	AX343247	AX343247 Sequence
13	16.2	46.3	36	6	AX078705	AX078705 Sequence
14	16.2	46.3	36	6	AX078728	AX078728 Sequence
15	16.2	46.3	36	6	AX078730	AX078730 Sequence
16	16.2	46.3	36	6	AX078732	AX078732 Sequence
17	16.2	46.3	53	6	AX328132	AX328132 Sequence
18	16.2	46.3	53	6	AX328132	AX328132 Sequence
19	16.2	46.3	53	6	AX328132	AX328132 Sequence
20	15.8	45.1	51	6	AX157590	AX157590 Sequence
21	15.6	44.6	60	6	AX350303	AX350303 Sequence
22	15.4	44.0	51	6	AX286077	AX286077 Sequence
23	15.4	44.0	80	6	AX286077	AX286077 Sequence
24	15.4	44.0	81	6	AX286077	AX286077 Sequence
25	15.4	44.0	81	6	AX286077	AX286077 Sequence
26	15.4	44.0	81	6	AX286077	AX286077 Sequence
27	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
28	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
29	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
30	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
31	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
32	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
33	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
34	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
35	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
36	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
37	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
38	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
39	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
40	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
41	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
42	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
43	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
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52	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
53	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
54	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
55	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
56	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
57	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
58	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
59	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
60	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
61	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
62	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
63	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
64	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
65	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
66	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
67	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
68	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
69	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
70	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
71	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
72	15.2	43.4	76	9	HS444349	HS444349 Homo sapi
73	15.2	43.4	76	9	HS444349	HS444349 Homo sapi

C 74	14	40.0	31	6	BD002521	BD002521 Gene comp	147	13.4	38.3	90	6	AX052940	AX052940 Sequence
C 75	14	40.0	33	5	AX004519	AX004519 Sequence	148	13.4	38.3	94	11	G38812	G38812 TA8 Plasmid
C 76	14	40.0	73	5	CARN2BD8	Z118729 Chlamydoel	149	13.4	38.3	95	11	HSPE14A08	AL0033613 H.sapiens
C 77	14	40.0	79	6	AR062559	AR062559 Sequence	150	13.4	38.3	100	9	AJ8122	AJ008122 Homo sapi
C 78	14	40.0	79	6	AR125962	AR125962 Sequence	151	13.4	38.3	100	12	SYNMISIGDC	M12053 Mouse Ig de
C 79	14	40.0	79	6	I47282	I47282 Sequence	152	13.2	37.7	20	6	AR002301	AR002301 Sequence
C 80	14	40.0	79	8	PKU240499	AJ240499 Physconia	153	13.2	37.7	20	6	AR053152	AR053152 Sequence
C 81	14	40.0	81	14	AF227771	AF227771 Hepatitis	154	13.2	37.7	20	6	AR053152	AR053152 Sequence
C 82	14	40.0	82	3	PGCHOMEOF	L119179 Phagocata w	155	13.2	37.7	20	6	AR171473	AR171473 Sequence
C 83	14	40.0	86	6	AR042768	AR042768 Sequence	156	13.2	37.7	21	6	AR112357	AR112357 Sequence
C 84	14	40.0	96	6	A23312	A23312 oligonucleot	157	13.2	37.7	21	6	AR163672	AR163672 Sequence
C 85	14	40.0	96	6	AR013739	AR013739 Sequence	158	13.2	37.7	21	6	AX048866	AX048866 Sequence
C 86	13.8	39.4	30	6	AR077753	AR077753 Sequence	159	13.2	37.7	23	6	AR003588	AR003588 Sequence
C 87	13.8	39.4	31	6	AX053547	AX053547 Sequence	160	13.2	37.7	25	6	A46987	A46987 Sequence
C 88	13.8	39.4	44	6	AX343236	AX343236 Sequence	161	13.2	37.7	25	6	AR102350	AR102350 Sequence
C 89	13.8	39.4	44	6	AX353884	AX353884 Sequence	162	13.2	37.7	27	6	AX052685	AX052685 Sequence
C 90	13.8	39.4	50	6	AR032920	AR032920 Sequence	163	13.2	37.7	28	6	I59697	I59697 Sequence
C 91	13.8	39.4	50	6	I29660	I29660 Sequence	164	13.2	37.7	28	6	I59703	I59703 Sequence
C 92	13.8	39.4	50	6	I91334	I91334 Sequence	165	13.2	37.7	33	6	I11713	I11713 Sequence
C 93	13.8	39.4	51	6	AX157821	AX157821 Sequence	166	13.2	37.7	41	6	AR002417	AR002417 Sequence
C 94	13.8	39.4	51	6	AX159285	AX159285 Sequence	167	13.2	37.7	41	6	AR034607	AR034607 Sequence
C 95	13.8	39.4	51	6	AX203685	AX203685 Sequence	168	13.2	37.7	41	6	I66285	I66285 Sequence
C 96	13.8	39.4	59	6	AX011351	AX011351 Sequence	169	13.2	37.7	41	6	I79897	I79897 Sequence
C 97	13.8	39.4	69	6	AF189384	AF189384 Homo sapi	170	13.2	37.7	42	6	I08595	I08595 Sequence
C 98	13.8	39.4	81	6	I19318	I19318 Sequence	171	13.2	37.7	42	10	MUSIDJCK	I16798 Mus muscullu
C 99	13.8	39.4	81	14	AB001394	AB001394 Hepatitis	172	13.2	37.7	45	6	I11712	I11712 Sequence
C 100	13.8	39.4	81	14	AB001396	AB001396 Hepatitis	173	13.2	37.7	50	6	AR032967	AR032967 Sequence
C 101	13.8	39.4	81	14	AF207432	AF207432 Hepatitis	174	13.2	37.7	50	6	AR032968	AR032968 Sequence
C 102	13.8	39.4	96	6	AX354334	AX354334 Sequence	175	13.2	37.7	50	6	I29707	I29707 Sequence
C 103	13.8	39.4	100	6	AR142893	AR142893 Sequence	176	13.2	37.7	50	6	I29708	I29708 Sequence
C 104	13.6	38.9	31	6	AR112220	AR112220 Sequence	177	13.2	37.7	50	6	I91381	I91381 Sequence
C 105	13.6	38.9	31	6	AR112222	AR112222 Sequence	178	13.2	37.7	50	6	I91382	I91382 Sequence
C 106	13.6	38.9	31	6	AR149262	AR149262 Sequence	179	13.2	37.7	50	14	AF189252	AF189252 Porcine
C 107	13.6	38.9	31	6	AR149264	AR149264 Sequence	180	13.2	37.7	51	6	A46976	A46976 Sequence
C 108	13.6	38.9	32	6	I26213	I26213 Sequence	181	13.2	37.7	51	6	AR102344	AR102344 Sequence
C 109	13.6	38.9	40	6	AR148771	AR148771 Sequence	182	13.2	37.7	51	6	AX141064	AX141064 Sequence
C 110	13.6	38.9	42	6	AR100954	AR100954 Sequence	183	13.2	37.7	51	6	AX146934	AX146934 Sequence
C 111	13.6	38.9	51	6	AX155976	AX155976 Sequence	184	13.2	37.7	51	6	AX159869	AX159869 Sequence
C 112	13.6	38.9	51	6	AX162402	AX162402 Sequence	185	13.2	37.7	51	6	AX161095	AX161095 Sequence
C 113	13.6	38.9	61	6	AR165812	AR165812 Sequence	186	13.2	37.7	51	6	AX161097	AX161097 Sequence
C 114	13.6	38.9	72	11	G70637	G70637 697352931FB	187	13.2	37.7	51	6	AX165559	AX165559 Sequence
C 115	13.6	38.9	76	14	FLAHAE	X65434 Influenza v	188	13.2	37.7	54	6	AR022588	AR022588 Sequence
C 116	13.6	38.9	81	9	HSBCL233	X65233 H.sapiens v	189	13.2	37.7	54	6	AR037603	AR037603 Sequence
C 117	13.6	38.9	81	9	S80450	S80450 V Delta 23-C	190	13.2	37.7	54	6	AR178061	AR178061 Sequence
C 118	13.6	38.9	87	3	SUPHISAALF	M25170 Sea urchin	191	13.2	37.7	57	9	H01086S07	H01086S07 Sequence
C 119	13.6	38.9	89	6	AR2518	AR2518 Sequence	192	13.2	37.7	60	6	E64748	E64748 Reagent for
C 120	13.6	38.9	91	9	HSBCL228	K65228 H.sapiens	193	13.2	37.7	61	1	AF209514	AF209514 Escherich
C 121	13.6	38.9	93	9	AF417181	AF417181 Macaca mu	194	13.2	37.7	62	6	AR040780	AR040780 Sequence
C 122	13.4	38.3	28	6	AR159831	AR159831 Sequence	195	13.2	37.7	69	5	RRN28D8	RRN28D8 Sequence
C 123	13.4	38.3	31	6	AX248432	AX248432 Sequence	196	13.2	37.7	72	5	RRN28D8	RRN28D8 Sequence
C 124	13.4	38.3	32	6	AX174814	AX174814 Sequence	197	13.2	37.7	78	10	MMCA2IV7	MMCA2IV7 Sequence
C 125	13.4	38.3	33	6	E51297	E51297 Novel G pro	198	13.2	37.7	78	10	MUSMTMTAA	MUSMTMTAA Sequence
C 126	13.4	38.3	33	6	E51118	E51118 Novel G pro	199	13.2	37.7	79	6	AR062564	AR062564 Sequence
C 127	13.4	38.3	50	6	AX199480	AX199480 Sequence	200	13.2	37.7	79	6	AR125968	AR125968 Sequence
C 128	13.4	38.3	50	6	AX199482	AX199482 Sequence	201	13.2	37.7	79	6	I47288	I47288 Sequence
C 129	13.4	38.3	50	6	AX199484	AX199484 Sequence	202	13.2	37.7	80	4	BTFTTIS1	BTFTTIS1 Sequence
C 130	13.4	38.3	50	6	AX287016	AX287016 Sequence	203	13.2	37.7	84	6	AR002356	AR002356 Sequence
C 131	13.4	38.3	51	6	AX159052	AX159052 Sequence	204	13.2	37.7	84	6	AR002385	AR002385 Sequence
C 132	13.4	38.3	51	6	AX159409	AX159409 Sequence	205	13.2	37.7	84	6	AR030859	AR030859 Sequence
C 133	13.4	38.3	51	6	AX191885	AX191885 Sequence	206	13.2	37.7	84	6	AR030888	AR030888 Sequence
C 134	13.4	38.3	51	6	AF254563	AF254563 Homo sapi	207	13.2	37.7	84	6	AR068254	AR068254 Sequence
C 135	13.4	38.3	54	6	E54538	E54538 Herpesvirus	208	13.2	37.7	84	6	AR068283	AR068283 Sequence
C 136	13.4	38.3	55	6	A75807	A75807 Sequence	209	13.2	37.7	84	6	I86805	I86805 Sequence
C 137	13.4	38.3	55	6	I73448	I73448 Sequence	210	13.2	37.7	84	6	I86834	I86834 Sequence
C 138	13.4	38.3	56	6	AX183555	AX183555 Sequence	211	13.2	37.7	84	6	AB0048534	AB0048534 Sequence
C 139	13.4	38.3	56	6	HSADDS07	AF000087 Homo sapi	212	13.2	37.7	85	10	MMCFYINT6	MMCFYINT6 Sequence
C 140	13.4	38.3	60	6	AX027956	AX027956 Sequence	213	13.2	37.7	86	6	E00062	E00062 DNA coding
C 141	13.4	38.3	60	12	AX028053	AX028053 Sequence	214	13.2	37.7	86	6	I02342	I02342 Sequence
C 142	13.4	38.3	69	6	AX287987	AX287987 Sequence	215	13.2	37.7	86	6	I07827	I07827 Sequence
C 143	13.4	38.3	69	6	AX287988	AX287988 Sequence	216	13.2	37.7	87	6	AR026137	AR026137 Sequence
C 144	13.4	38.3	75	9	HUMTF12	M13372 Human trans	217	13.2	37.7	90	1	VSHEMONT	X17305 Vltreoscill
C 145	13.4	38.3	78	3	AX013985	AX013985 Haichond	218	13.2	37.7	90	6	AX039250	AX039250 Sequence
C 146	13.4	38.3	79	9	HSRONP003	AF164635 Homo sapi	219	13.2	37.7	90	6	AX039490	AX039490 Sequence

C 220	13.2	37.7	90	6	AX134848	AX134848 Sequence	293	13	37.1	94	8	BVU35419	U35419 Beauveria v
C 221	13.2	37.7	90	6	AX134937	AX134937 Sequence	294	13	37.1	96	10	RNU78114	U78114 Rattus norv
C 222	13.2	37.7	90	6	AX135056	AX135056 Sequence	C 295	13	37.1	98	6	I08888	I08888 Sequence 6
C 223	13.2	37.7	99	9	HUMCG3A02	M10797 Human alpha	C 296	13	37.1	99	14	HIVFTRLH	M62311 Human Immun
C 224	13	37.1	27	6	AX174820	AX174820 Sequence	C 297	13	37.1	100	9	AR18154	AU008154 Homo sapi
C 225	13	37.1	29	6	AX343234	AX343234 Sequence	C 298	12.8	36.6	20	6	AR124970	AR124970 Sequence
C 226	13	37.1	29	6	AX353882	AX353882 Sequence	C 299	12.8	36.6	22	6	AR103422	AR103422 Sequence
C 227	13	37.1	30	6	AX148791	AX148791 Sequence	C 300	12.8	36.6	22	6	AR151630	AR151630 Sequence
C 228	13	37.1	30	6	AX148795	AX148795 Sequence	C 301	12.8	36.6	23	6	AR112025	AR112025 Sequence
C 229	13	37.1	32	6	AX280959	AX280959 Sequence	C 302	12.8	36.6	24	6	AR6988	AR6988 Sequence 28
C 230	13	37.1	33	9	HSAMW6B	X12101 H. sapiens (	C 303	12.8	36.6	24	6	AR102351	AR102351 Sequence
C 231	13	37.1	36	6	AR003789	AR003789 Sequence	C 304	12.8	36.6	24	6	AX291070	AX291070 Sequence
C 232	13	37.1	36	6	AR010125	AR010125 Sequence	C 305	12.8	36.6	25	6	AR089449	AR089449 Sequence
C 233	13	37.1	36	6	AR055331	AR055331 Sequence	C 306	12.8	36.6	25	6	EA1384	EA1384 Amino acid
C 234	13	37.1	36	6	AR141260	AR141260 Sequence	C 307	12.8	36.6	26	6	AX043858	AX043858 Sequence
C 235	13	37.1	36	6	AR141497	AR141497 Sequence	C 308	12.8	36.6	28	6	AR091051	AR091051 Sequence
C 236	13	37.1	36	6	111971	111971 Sequence 83	C 309	12.8	36.6	31	6	144031	144031 Sequence 5
C 237	13	37.1	36	6	140542	140542 Sequence 81	C 310	12.8	36.6	39	6	AR116097	AR116097 Sequence
C 238	13	37.1	37	6	126193	126193 Sequence 26	C 311	12.8	36.6	39	6	145596	145596 Sequence 9
C 239	13	37.1	41	6	AR009877	AR009877 Sequence	C 312	12.8	36.6	40	6	115380	115380 Sequence 2
C 240	13	37.1	45	6	AX214211	AX214211 Sequence	C 313	12.8	36.6	42	6	AR038910	AR038910 Sequence
C 241	13	37.1	46	6	A05126	A05126 Oligonucleo	C 314	12.8	36.6	43	6	134859	134859 Sequence 2
C 242	13	37.1	46	6	AX214194	AX214194 Sequence	C 315	12.8	36.6	45	6	AX082539	AX082539 Sequence
C 243	13	37.1	46	6	AX214196	AX214196 Sequence	C 316	12.8	36.6	45	6	AX239597	AX239597 Sequence
C 244	13	37.1	46	6	AX214197	AX214197 Sequence	C 317	12.8	36.6	48	6	AX284152	AX284152 Sequence
C 245	13	37.1	46	6	AX214198	AX214198 Sequence	C 318	12.8	36.6	48	10	MUSTIGHYS	M22389 Mouse Ig ge
C 246	13	37.1	46	6	AX214200	AX214200 Sequence	C 319	12.8	36.6	50	9	HUMTCCV14	L39471 Homo sapien
C 247	13	37.1	46	6	AX214202	AX214202 Sequence	C 320	12.8	36.6	51	6	AX156887	AX156887 Sequence
C 248	13	37.1	46	6	AX214210	AX214210 Sequence	C 321	12.8	36.6	51	6	AX157569	AX157569 Sequence
C 249	13	37.1	48	6	AR024318	AR024318 Sequence	C 322	12.8	36.6	51	6	AX158218	AX158218 Sequence
C 250	13	37.1	48	6	AR035498	AR035498 Sequence	C 323	12.8	36.6	51	6	AX160961	AX160961 Sequence
C 251	13	37.1	48	6	AR045171	AR045171 Sequence	C 324	12.8	36.6	51	6	AX161093	AX161093 Sequence
C 252	13	37.1	48	6	BD011395	BD011395 Chimeric	C 325	12.8	36.6	51	6	AX161094	AX161094 Sequence
C 253	13	37.1	48	6	EA3865	EA3865 Chimeric an	C 326	12.8	36.6	51	6	AX161270	AX161270 Sequence
C 254	13	37.1	48	6	159449	159449 Sequence 7	C 327	12.8	36.6	51	6	AX161858	AX161858 Sequence
C 255	13	37.1	48	23	E11162	E11162 Oligonucleo	C 328	12.8	36.6	51	6	AX162652	AX162652 Sequence
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C 260	13	37.1	51	6	AX158871	AX158871 Sequence	C 333	12.8	36.6	51	6	AX141066	AX141066 Sequence
C 261	13	37.1	51	6	AX158873	AX158873 Sequence	C 334	12.8	36.6	54	6	AX146936	AX146936 Sequence
C 262	13	37.1	51	6	AX158874	AX158874 Sequence	C 335	12.8	36.6	59	6	AB010680	AB010680 Homo sapi
C 263	13	37.1	51	6	AX162070	AX162070 Sequence	C 336	12.8	36.6	60	6	A93059	A93059 Sequence 36
C 264	13	37.1	54	6	A38936	A38936 Sequence 23	C 337	12.8	36.6	60	6	AR009394	AR009394 Sequence
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C 267	13	37.1	56	6	123354	123354 Sequence 8	C 340	12.8	36.6	60	6	E65258	E65258 Mutant of E
C 268	13	37.1	60	6	AR051733	AR051733 Sequence	C 341	12.8	36.6	65	9	AB032807	AB032807 Homo sapi
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C 272	13	37.1	70	11	HUMSMX666	L24887 Human Chrom	C 345	12.8	36.6	69	1	RG23SMB16	Y09756 R.gallegae 2
C 273	13	37.1	71	6	123355	123355 Sequence 9	C 346	12.8	36.6	70	10	MMVIMV60	X89177 M.musculus
C 274	13	37.1	72	6	AR140803	AR140803 Sequence	C 347	12.8	36.6	71	5	LRN28D8	Z18735 Limanda 11m
C 275	13	37.1	72	6	AX150235	AX150235 Sequence	C 348	12.8	36.6	71	6	AB2520	AB2520 Sequence 23
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C 282	13	37.1	73	9	HUMMACAB	L37714 Homo sapien	C 355	12.8	36.6	79	6	104459	104459 Sequence 57
C 283	13	37.1	78	10	MUSMWTABA	M36651 Mouse mitoc	C 356	12.8	36.6	84	6	AR018996	AR018996 Sequence
C 284	13	37.1	81	6	AR127695	AR127695 Sequence	C 357	12.8	36.6	84	6	AR037739	AR037739 Sequence
C 285	13	37.1	81	6	175364	175364 Sequence 11	C 358	12.8	36.6	84	6	133747	133747 Sequence 43
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C 370	12.6	36.0	24	6	AX292404	AX292404 Sequence	443	12.6	36.0	86	5	S76800	S76800 anion excha
C 371	12.6	36.0	24	6	E59935	E59935 Human male-	444	12.6	36.0	94	8	AF372982	AF372982 Pneumocys
C 372	12.6	36.0	27	6	AX116972	AX116972 Sequence	445	12.6	36.0	96	14	H1VLRID	M62307 Human Immun
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C 377	12.6	36.0	30	6	A62202	A62202 Sequence 96	450	12.6	36.0	100	6	AR130585	AR130585 Sequence
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C 379	12.6	36.0	30	6	AX022426	AX022426 Sequence	452	12.6	36.0	100	6	AR142895	AR142895 Sequence
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C 391	12.6	36.0	36	6	AR171666	AR171666 Sequence	464	12.4	35.4	24	6	A13729	A13729 Oligonucleot
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C 400	12.6	36.0	41	6	AX074210	AX074210 Sequence	473	12.4	35.4	27	6	I20953	I20953 Sequence 20
C 401	12.6	36.0	41	6	AX299784	AX299784 Sequence	474	12.4	35.4	30	6	AR160339	AR160339 Sequence
C 402	12.6	36.0	41	6	AX327075	AX327075 Sequence	475	12.4	35.4	30	6	E27464	E27464 Novel gene
C 403	12.6	36.0	41	6	AX327076	AX327076 Sequence	476	12.4	35.4	31	6	A06219	A06219 Synthetic D
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C 421	12.6	36.0	51	6	AX199266	AX199266 Sequence	494	12.4	35.4	45	9	H0MTGRABH	L06994 Human 19 re
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Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 3  
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DEFINITION Sequence 919 from Patent WO0140521.  
ACCESSION AX157591  
VERSION AX157591.1 GI:14538922  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Shinkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 919 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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RESULT 4  
ARI20506/c  
LOCUS ARI20506 38 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 382 from patent US 6159469.  
ACCESSION ARI20506  
VERSION ARI20506.1 GI:14104082  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Choi,I.G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,  
Fannon,M.R. and Rosen,C.A.  
TITLE Streptococcus pneumoniae antigens and vaccines  
JOURNAL Patent: US 6159469-A 382 12-DEC-2000;  
Location/Qualifiers  
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Query Match 49.1%; Score 17.2; DB 6; Length 38;  
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Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 5  
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LOCUS HSA344350 75 bp DNA linear PRI 06-SEP-2001  
DEFINITION Homo sapiens partial IGDH3-9 gene segment, isolate case6-cell1520.  
ACCESSION AJ344350  
VERSION AJ344350.1 GI:15528515  
KEYWORDS IGDH3-9 gene.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Braeuninger A., Spieker,T., Willenbrock,K., Gaulard,P.,  
Wacker,H.H., Rajewsky,K., Hansmann,M.L. and Kuipers,R.  
TITLE Survival and clonal expansion of mutating 'forbiden'  
(immunoglobulin receptor-deficient) Epstein-Barr virus-infected B cells in angioimmunoblastic T cell lymphoma  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 75)  
AUTHORS Braeuninger A.  
TITLE Direct Submission  
JOURNAL Submitted (28-AUG-2001) Braeuninger A., Pathology, University of Frankfurt, Theodor-Stern-Kai 7, 60590, GERMANY  
FEATURES  
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Db 7 AGCTTAGAATGAGCTCTGTCTACTGTGG 36

RESULT 6  
HSIGD2105  
LOCUS HSIGD2105 88 bp DNA linear PRI 02-JUN-1999  
DEFINITION H.sapiens germline immunoglobulin heavy chain, diversity region (021/0.5).  
ACCESSION X93613  
VERSION X93613.1 GI:1089851  
KEYWORDS antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Bulwela,L., Albertson,D.G., Sherrington,P., Rabbitts,P.H.,  
Spurr,N. and Rabbitts,F.H.  
TITLE The use of chromosomal translocations to study human immunoglobulin gene organization: Mapping D-H segments within 35 kb of the C-mu gene and identification of a new D-H locus  
JOURNAL EMBO J. 7, 2003-2010 (1988)  
MEDLINE 88328988  
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source Location/Qualifiers  
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 Db 1 AGGTTAGAAATGAGCTGCTGTCTGCTG 30  
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 LOCUS Human Ig rearranged heavy-chain gene D-J region, partial cds.  
 ACCESSION M36099.1 GI:184805  
 VERSION M36099.1 GI:184805  
 KEYWORDS D-region; J-region; immunoglobulin heavy chain; processed gene.  
 SOURCE Human acute lymphoblastic leukemia B-cell line DNA, from patient TD.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 100)  
 AUTHORS Bird,J., Gallil,N., Link,M., Stites,D. and Sklar,J.  
 TITLE Continuing rearrangement but absence of somatic hypermutation in immunoglobulin genes of human B cell precursor leukemia  
 JOURNAL J. Exp. Med. 168 (1), 229-245 (1988)  
 MEDLINE 88286083  
 FEATURES Location/Qualifiers  
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 Best Local Similarity 73.3%; Pred. No. 1.6e+04;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 atgtctagaatgggagtggtcactctg 31  
 Db 4 AGGTTAGAAATGAGCTGCTGTCTGCTG 33  
 RESULT 8  
 AR035931 42 bp DNA linear PAT 29-SEP-1999  
 LOCUS AR035931  
 DEFINITION Sequence 124 from patent US 5871962.  
 ACCESSION AR035931  
 VERSION AR035931.1 GI:5952599  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Bukh,J., Miller,R.H. and Purcell,J.R.H.

TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods  
 JOURNAL Patent: US 5871962-A 124 15-FEB-1999;  
 FEATURES Location/Qualifiers  
 source 1..42  
 /organism="unknown"  
 BASE COUNT 7 a 13 c 13 g 9 t  
 ORIGIN  
 Query Match 48.0%; Score 16.8; DB 6; Length 42;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+04;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 catgtctagaatgggagtggtcactc 28  
 Db 30 CATGTCGAGAAAGGCTGTGGGACCTC 3  
 RESULT 9  
 I20167/c 42 bp DNA linear PAT 07-OCT-1996  
 LOCUS I20167  
 DEFINITION Sequence 124 from patent US 5514539.  
 ACCESSION I20167  
 VERSION I20167.1 GI:1600522  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Bukh,J., Miller,R.H. and Purcell,J.R.H.  
 TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines  
 JOURNAL Patent: US 5514539-A 124 07-MAY-1996;  
 MEDLINE Location/Qualifiers  
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 BASE COUNT 7 a 13 c 13 g 9 t  
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 Best Local Similarity 75.0%; Pred. No. 2.7e+04;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 catgtctagaatgggagtggtcactc 28  
 Db 30 CATGTCGAGAAAGGCTGTGGGACCTC 3  
 RESULT 10  
 HUMIGBU 88 bp DNA linear PRI 27-APR-1993  
 LOCUS HUMIGBU  
 DEFINITION Human agammaglobulinemia-associated dysfunctional Ig rearranged heavy chain D-region (D-XPI-J-H5) gene, clone lambda-XPB3.3.  
 ACCESSION M20417  
 VERSION M20417.1 GI:185152  
 KEYWORDS C-region; D-region; J-region; immunoglobulin heavy chain; processed gene.  
 SOURCE Human bone marrow Epstein-Barr virus transformed precursor B cell line DNA, clone lambda-XPB3.3, from a patient with X-linked agammaglobulinemia.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 88)  
 AUTHORS Ichihara,Y., Matsuo,K.H., Tsuge,I., Okada,J.-I., Torii,S., Yasui,H. and Kurosawa,Y.  
 TITLE Abnormalities in DNA rearrangements of immunoglobulin gene loci in precursor B cells derived from X-linked agammaglobulinemia patient and a severe combined immunodeficiency patient

JOURNAL Immunogenetics 27, 330-337 (1988)  
MEDLINE 88186098  
FEATURES  
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ORIGIN Chromosome 14q32.3.

Query Match 48.0%; Score 16.6; DB 9; Length 88;  
Best Local Similarity 75.0%; Pred. No. 2.4e+04;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 2 GTTGAATGAGTCTGTCTCCTCTG 29

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AX343247 38 bp DNA linear PAT 01-FEB-2002  
LOCUS Sequence 3 from Patent EP1170379.  
ACCESSION AX343247  
VERSION AX343247.1 GI:18491602  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Gut,I.G., Lechner,D. and Sauer,S.  
TITLE Sample generation for genotyping by mass spectrometry  
JOURNAL Patent: EP 1170379-A 3 09-JAN-2002;  
Centre National de Genotypage (FR)  
FEATURES  
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BASE COUNT 9 a 11 c 12 g 6 t  
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Best Local Similarity 71.0%; Pred. No. 3.3e+04;  
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 6 CCTGACTCCACGAGGAGGAGGTCCTCGG 36

RESULT 12  
AX351627 38 bp DNA linear PAT 06-FEB-2002  
LOCUS Sequence 3 from Patent WO0200931.  
ACCESSION AX351627  
VERSION AX351627.1 GI:18616910  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Gut,I.G., Lechner,D. and Sauer,S.  
TITLE Sample generation for genotyping by mass spectrometry  
JOURNAL Patent: WO 0200931-A 3 03-JAN-2002;  
Centre National de Genotype (FR)  
FEATURES  
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            /db\_xref="taxon:9606"  
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ORIGIN

Query Match 47.4%; Score 16.6; DB 6; Length 38;  
Best Local Similarity 71.0%; Pred. No. 3.3e+04;  
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 catgtctagaatgggagtggtcactctg 31  
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Db 6 CCTGACTCCACGAGGAGGAGGTCCTCGG 36

RESULT 13  
AX078705/c 36 bp DNA linear PAT 22-FEB-2001  
LOCUS Sequence 1 from Patent WO0107573.  
ACCESSION AX078705  
VERSION AX078705.1 GI:13158329  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequence.

REFERENCE  
AUTHORS Hauer,B., Schmid,R.D. and Schwaneberg,U.  
TITLE Electron donor system for enzymes and its use for the biochemical conversion of substrates  
JOURNAL Patent: WO 0107573-A 1 01-FEB-2001;  
BASF AKTIENGESELLSCHAFT (DE)  
FEATURES  
    source 1. .36  
            /organism="synthetic construct"  
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            /note="Oligonukleotid fuer genomische Bacillus megaterium-DNA"  
BASE COUNT 15 a 6 c 9 g 6 t  
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Query Match 46.3%; Score 16.2; DB 6; Length 36;  
Best Local Similarity 72.4%; Pred. No. 4.9e+04;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 catgtctagaatgggagtggtcactct 29  
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Db 34 CATTCTTAATGTGATGGATCCCTCT 6

RESULT 14  
AX078728 36 bp DNA linear PAT 22-FEB-2001  
LOCUS Sequence 24 from Patent WO0107573.  
ACCESSION AX078728  
VERSION AX078728.1 GI:13158352  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequence.

REFERENCE  
AUTHORS Hauer,B., Schmid,R.D. and Schwaneberg,U.  
TITLE Electron donor system for enzymes and its use for the biochemical conversion of substrates  
JOURNAL Patent: WO 0107573-A 24 01-FEB-2001;  
BASF AKTIENGESELLSCHAFT (DE)  
FEATURES  
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BASE COUNT 15 a 6 c 9 g 6 t  
ORIGIN

Query Match 46.3%; Score 16.2; DB 6; Length 36;

Best Local Similarity 72.4%; Pred. NO. 4.9e+04;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 catgtctagaatggtggtcactct 29

Db 34 CATTCCTTAATGTCATGGATCCCTCT 6

RESULT 15

LOCUS	AX078730	36 bp	DNA	linear	PAT 22-FEB-2001
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DEFINITION	Sequence 26 from Patent WO0107573.
ACCESSION	AY079730

VERSION AX078730.1 GI:13158354

**KEYWORDS** syntactic construct source

synthetic construct.

artificial sequence.

REFERENCE 1 (bases 1 to 36)

**AUTHORS** Hauer, B., Schmid, R. L.

TITLE
Electron donor systems

conversion of substr  
patent: WO 0107573-A

JOURNAL  
FALL: WO 010/3/3-A  
BASE AKTIENGESellschaft

FEATURES	PRICE ANALYSIS	LOCATION/QUALITY
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/db\_xref="t

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BASE COUNT      15 a      6 c      /note=" 011
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BASE COUNT	13 d	6 c
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Query Match	Score	DB	Length
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Best Local Similarity 72.4%; Pred. NO. 4.9e+04;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 34 CATTCTTAATTGTCATGGATCCCTCT 6

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Search completed: June 22, 2002, 05:32:11
Job time: 5091 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:39:59 ; Search time 369.89 Seconds  
(without alignments)  
162.459 Million cell updates/sec

Title: US-09-927-267-13

Perfect score: 35

Sequence: 1 catgtctagaatggggatggtgctactctgacct 35

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 2046006

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

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24: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.2	52.0	46	7	AA60796
2	17.6	50.3	51	22	AA173976
3	17.6	50.3	51	22	AA173978
4	17.2	49.1	38	19	AAV39899
5	17	48.6	58	18	AAV92889
6	16.8	48.0	42	16	AA083917
7	16.8	48.0	42	17	AA176677
8	16.4	46.9	50	22	AA133984
9	16.2	46.3	36	22	AA262335

C 10	16.2	46.3	36	22	AA26258
C 11	16.2	46.3	36	22	AA26260
C 12	16.2	46.3	36	22	AA26262
C 13	16.2	46.3	36	22	AA263314
C 14	16	45.7	51	22	AA173977
C 15	16	45.7	51	22	AA173979
C 16	16	45.7	93	22	ABA75975
C 17	16	45.7	93	22	ABA40538
C 18	16	45.7	93	22	AA24653
C 19	16	45.7	93	22	AA24653
C 20	16	45.7	93	22	AA24653
C 21	16	45.7	93	22	AA24653
C 22	15.6	44.6	60	24	ABA02187
C 23	15.6	44.6	88	15	AA074766
C 24	15.6	44.6	88	15	AA074766
C 25	15.4	44.0	51	22	AA175673
C 26	15.4	44.0	81	16	AA26266
C 27	15.4	44.0	82	21	AA26266
C 28	15.4	44.0	86	21	AA26266
C 29	15.4	44.0	98	21	AA26266
C 30	15.4	44.0	100	20	AA26266
C 31	15.2	43.4	47	12	AA010271
C 32	15.2	43.4	51	22	AA010271
C 33	15.2	43.4	86	22	AA010271
C 34	15.2	43.4	86	22	AA010271
C 35	15.2	43.4	86	22	AA010271
C 36	15	42.9	25	21	AA26054
C 37	15	42.9	32	16	AA087423
C 38	15	42.9	32	16	AA087423
C 39	14.8	42.3	51	22	AA269466
C 40	14.8	42.3	51	22	AA269466
C 41	14.8	42.3	51	22	AA269466
C 42	14.8	42.3	51	22	AA269466
C 43	14.8	42.3	51	22	AA269466
C 44	14.8	42.3	51	22	AA269466
C 45	14.8	42.3	51	22	AA269466
C 46	14.8	42.3	51	22	AA269466
C 47	14.8	42.3	51	22	AA269466
C 48	14.8	42.3	51	22	AA269466
C 49	14.8	42.3	51	22	AA269466
C 50	14.8	42.3	51	22	AA269466
C 51	14.8	42.3	51	22	AA269466
C 52	14.8	42.3	51	22	AA269466
C 53	14.8	42.3	51	22	AA269466
C 54	14.6	41.7	21	13	AA028770
C 55	14.6	41.7	21	13	AA028770
C 56	14.6	41.7	21	13	AA028770
C 57	14.6	41.7	21	13	AA028770
C 58	14.6	41.7	21	13	AA028770
C 59	14.6	41.7	21	13	AA028770
C 60	14.6	41.7	21	13	AA028770
C 61	14.6	41.7	21	13	AA028770
C 62	14.6	41.7	21	13	AA028770
C 63	14.6	41.7	21	13	AA028770
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C 67	14.6	41.7	21	13	AA028770
C 68	14.6	41.7	21	13	AA028770
C 69	14.6	41.7	21	13	AA028770
C 70	14.6	41.7	21	13	AA028770
C 71	14.6	41.7	21	13	AA028770
C 72	14.6	41.7	21	13	AA028770
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C 74	14.4	41.1	24	19	AAV02967
C 75	14.4	41.1	24	19	AAV02967
C 76	14.4	41.1	24	19	AAV02967
C 77	14.4	41.1	24	19	AAV02967
C 78	14.4	41.1	24	19	AAV02967
C 79	14.4	41.1	24	19	AAV02967
C 80	14.4	41.1	24	19	AAV02967
C 81	14.4	41.1	24	19	AAV02967
C 82	14.4	41.1	24	19	AAV02967

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B. megaterium BM-3  
B. megaterium BM-3  
Human neutropilin-1  
Human silent SNP c  
Human silent SNP c  
Human foetal liver  
Probe #19004 for g  
Human brain expres  
Human bone marrow  
Probe #17596 for g  
Arabidopsis ubiquitin  
Human prepro-eryth  
Human silent SNP c  
PCR primer 2 used  
HIV-1 reverse tran  
Human secreted pro  
HALO1, fragment of  
Human secreted pro  
Probe A(11) for bo  
Human SNP oligonuc  
Human brain expres  
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Probe #19919 used  
Probe for mouse ML  
Human GRK antisens  
Human SNP flanking  
Ig gamma 5' PCR pr  
Human silent SNP c  
E3-b1 primer used  
Human foetal liver  
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Probe #21746 used  
Human breast cell  
Human foetal liver  
Probe #13502 for g  
Human brain expres  
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Probe #12840 for g  
Probe #16891 used  
Probe #8562 used c  
HNA class II gene  
Human pax protein  
Probe specific for  
DNA encoding class  
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DNA encoding class  
DNA encoding class  
Human PRO109 hydr  
DNA encoding class  
Probe used to delete  
Human SNP involin  
Human silent SNP c  
Human secreted pro  
Human HIV/tumorige  
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Human biallelic ma  
Hepatitis GB virus  
Androgen receptor  
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Human PRO245 hydr  
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Probe used to isol













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959 12.2 34.9 71 18 AAT57859 L-selectin family
c 960 12.2 34.9 71 18 AAT57830 L-selectin family
961 12.2 34.9 72 22 AAT78935 cDNA encoding rat
962 12.2 34.9 73 16 AAO99756 Pseudomonas ergino
c 963 12.2 34.9 73 17 AAT71363 Red blood cell gho
964 12.2 34.9 74 11 AAO03841 Synthetic sequence
965 12.2 34.9 74 11 AAO03840 Synthetic sequence
966 12.2 34.9 74 11 AAO03839 Synthetic sequence
967 12.2 34.9 74 22 AAS43691 Corneodesmosin sin
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c 971 12.2 34.9 77 18 AAT79108 RNA ligand to HIV-
c 972 12.2 34.9 77 22 ABA70048 Human foetal liver
c 973 12.2 34.9 77 22 AAK18257 Human brain expres
c 974 12.2 34.9 77 22 AAK44153 Human bone marrow
c 975 12.2 34.9 77 22 AAK44538 Human bone marrow
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c 978 12.2 34.9 77 22 AAI50526 Probe #19212 used
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981 12.2 34.9 79 22 ABA65156 Human foetal liver
982 12.2 34.9 79 22 ABA32258 Probe #10724 for g
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984 12.2 34.9 79 22 AAK3314 Human bone marrow
985 12.2 34.9 79 22 AAI20127 Probe #10060 for g
986 12.2 34.9 79 22 AAI45327 Probe #14013 used
987 12.2 34.9 80 9 AAN80462 Expression-control
988 12.2 34.9 81 12 AAO13139 Hybrid promoter.
989 12.2 34.9 81 12 AAO14475 Hybrid of T3 phage
990 12.2 34.9 81 16 AAT06268 HIV-1 reverse tran
991 12.2 34.9 81 16 AAT06269 HIV-1 reverse tran
992 12.2 34.9 82 20 AAX32349 Artificial NS4 mos
c 993 12.2 34.9 82 24 AAD22604 BVDV CP7 cDNA muta
994 12.2 34.9 83 22 AAH28258 Oligonucleotide en
995 12.2 34.9 85 4 AAN30119 Sequence of the tr
996 12.2 34.9 85 22 AAG89215 Human brain T calc
997 12.2 34.9 86 22 ABA50507 Human breast cell
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## ALIGNMENTS

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ID AAN60796 standard; DNA; 46 BP.
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XX AAN60796;
AC
XX 01-JUL-1991 (first entry)
DT
XX
XX Sequence of probe substantially homologous with the DOB gene of the
DE HLA.
XX
XX Probe; hybridisation; diabetes; ss.
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XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT misc-feature /*tag= a
FT /*note= "also claimed as a probe"
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XX W08607464-A.
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XX 18-DEC-1986.
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XX 13-JUN-1986; 86WO-0001292.
XX
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PR 14-JUN-1985; 85US-0745321.
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XX (GENE-) GENETIC SYST CORP.
XX
XX Nepom GT, Nepom BS, Nelson KA;
XX
XX WPI; 1986-34665/52.
XX
XX
XX Detection of alleles associated with increased risk of diabetes -
PT using two different specified monoclonal antibodies
XX
XX
XX Claim 15; Page 19; 20pp; English.
XX
XX The probes are used in a method for identifying individuals at
CC increased risk of diabetes. The probe can be labelled with a
CC radioisotope or an enzyme.
XX
XX
XX Sequence 46 BP; 12 A; 19 C; 10 G; 5 T; 0 other;
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Query Match 52.0%; Score 18.2; DB 7; Length 46;
Best Local Similarity 74.2%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 3 tgcctagaatgggagatgggctactctggac 33
DB 34 TGTCTCGATGGGAGATGTCATCTGTGGGC 4
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ID AAT73976 standard; DNA; 51 BP.
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XX AAT73976;
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AC
XX 09-NOV-2001 (first entry)
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DT
XX Human silent SNP containing nucleic acid SEQ:917.
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DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
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KW protein therapy; vaccine; probe; diagnostic assay; detection;
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KW quantitation; restorative therapy; polymorphic; ds.
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OS
XX
XX W0200140521-A2.
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```
XX
XX 07-JUN-2001.
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XX
XX 30-NOV-2000; 2000WO-US32758.
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XX
XX 30-NOV-1999; 99US-0168138.
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XX
XX 29-NOV-2000; 2000US-0726173.
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XX
XX (CURA-) CURAGEN CORP.
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XX
XX Shinkets RA, Leach M;
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XX
XX WPI; 2001-356160/37.
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XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
```

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PS
XX Claim 1; Page 334; 2653pp; English.
```

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XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
```

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XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
```

```
XX AAM53114 to AAM53329 represent peptides related to human polymorphic
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```
XX polynucleotide sequences. The sequences can be used in gene and protein
```

```
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
```

```
CC them may be used in the prevention, diagnosis and treatment of diseases
```

```
CC associated with inappropriate expression of polymorphic polypeptides.
```

```
CC For example, (I) may be used to treat disorders by rectifying mutations
```



CC or deletions in a patient's genome that affect the activity of  
CC polypeptides by expressing inactive proteins or to supplement the  
CC patients own production of polypeptide. Additionally, (1) and its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids  
CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (1) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.  
XX  
SO Sequence 51 BP; 6 A; 20 C; 19 G; 6 T; 0 other;

Query Match 50.3%; Score 17.6; DB 22; Length 51;  
Best Local Similarity 71.9%; Pred. No. 4.3e+02;  
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 3 tgtctagaatgggagtggtcactctgacc 34  
||| ||||| ||||| ||| ||| |||  
Db 12 tgcctatgtctgggacggcgccctcagttcc 43

RESULT 3  
AA173978  
ID AA173978 standard; DNA: 51 BP.

AC AA173978:

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:919.

DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140531-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US32758.

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

PT therapy -

XX Claim 1; Page 334; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

CC AA53114 to AA53129 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (1) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides.

CC For example, (1) may be used to treat disorders by rectifying mutations

CC or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the

CC patients own production of polypeptide. Additionally, (1) and its

CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids

CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (1) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.  
XX  
SO Sequence 51 BP; 6 A; 22 C; 17 G; 6 T; 0 other;

Query Match 50.3%; Score 17.6; DB 22; Length 51;  
Best Local Similarity 71.9%; Pred. No. 4.3e+02;  
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 3 tgtctagaatgggagtggtcactctgacc 34  
||| ||||| ||||| ||| ||| |||  
Db 10 tgcctatgtctgggacggcgccctcagttcc 41

RESULT 4  
AAV39899/C  
ID AAV39899 standard; DNA: 38 BP.

AC AAV39899:

DT 02-OCT-1998 (first entry)

XX Streptococcus pneumoniae ORF cloning primer SEQ ID NO:382.

DE Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;

KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.

XX Synthetic.

OS Streptococcus pneumoniae.

XX WO9818930-A2.

PD 07-MAY-1998.

PF 30-OCT-1997; 97WO-US19422.

PR 31-OCT-1996; 96US-0029960.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Hromocky J A, Johnson LS, Kunsch CA;

DR WPI; 1998-272224/24.

XX Nucleic acid encoding antigenic peptide(s) from Streptococcus

PT pneumoniae - or their epitope-containing fragments, useful in

PT protective or therapeutic vaccines, and for diagnosis

PT Example 1; Page 108; 118pp; English.

XX The present sequence represents a cloning primer used in an example from

CC the present invention which describes proteins from Streptococcus

CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae

CC proteins can be useful in vaccines for inducing protective antibodies

CC against Streptococcus pneumoniae, for treatment or prevention of

CC infection e.g. pneumonia, otitis media or meningitis. Probes based on

CC the nucleic acids are used to detect Streptococcus infection (by usual

CC hybridisation or amplification methods), also for isolating

CC Streptococcus genes or their allelic variants. The proteins can be used

CC similarly to detect specific antibodies in standard immunoassays,

CC especially for diagnosing or monitoring infections. Antibodies which

CC bind the proteins are used to detect corresponding antigens, to purify

CC the proteins and for passive immunisation (optionally coupled to a

CC toxin). Vaccines are administered, e.g. by injection, orally or through

CC the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.

CC The cloning primers used in the present invention are given in AAV27437

CC to AAV27562 and AAV39870 to AAV39969.



XX OS Synthetic.  
XX PN MO9605315-A2.  
XX PD 22-FEB-1996.  
XX PF 15-AUG-1995; 95MO-US10398.  
XX PR 15-AUG-1994; 94US-0290665.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI (USSH ) US SEC DEPT HEALTH.  
XX PI Bukh J, Miller RH, Purcell RH;  
XX DR WPI; 1996-139709/14.  
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins -  
XX PT used to determine HCV genotype and as vaccines against HCV infection  
XX PS Disclosure; Page 229; 340pp; English.  
XX CC AAT16662-T16688 are primers derived from a set of 51 different HCV  
XX CC EI (envelope-1) gene isolates that are useful for detecting the  
XX CC presence of HCV in a sample, the primers are genotype-specific and  
XX CC so are also useful for genotyping HCV CDNAs. Proteins encoded by HCV  
XX CC EI CDNAs can be used in vaccines for immunising against HCV infection.  
XX CC The proteins may also be used to detect antibodies against HCV in  
XX CC serum, saliva, lymphocytes or other mononuclear cells. The antibodies  
XX CC may be used in the prevention of HCV infection.  
XX SQ Sequence 42 BP; 7 A; 13 C; 13 G; 9 T; 0 other:  
  
Query Match 48.0%; Score 16.8; DB 17; Length 42;  
Best Local Similarity 75.0%; Pred. No. 8.9e+02;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
OY 1 catgtctagaatgggagtggtcactc 28  
||||| ||||| ||||| ||||| |||||  
Db 30 CATGTCGAGAAAGGCTGTGGGACCTC 3  
  
RESULT 8  
AAL33984/c  
ID AAL33984 standard; DNA: 50 BP.  
XX AC AAL33984;  
XX DT 24-JAN-2002 (first entry)  
XX DE Human SNP oligonucleotide #7192.  
XX XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;  
XX KM neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
XX KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX KM multifactorial disease; autoimmune disease; infection;  
XX KM nervous system disease; ss.  
XX XX  
XX OS Homo sapiens.  
XX PN WO200147944-A2.  
XX PD 05-JUL-2001.  
XX PF 28-DEC-2000; 2000MO-US35498.  
XX PR 28-DEC-1999; 99US-0173419.  
XX PR 27-DEC-2000; 2000US-0173419.

XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI; 2001-465210/50.  
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.  
XX PT cancer, autoimmune diseases and infections -  
XX PS Claim 1; Page 3450; 4143pp; English.  
XX CC The present invention relates to oligonucleotides encoding polymorphic  
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX CC histones, kinases, colony stimulating factors, complement related  
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
XX CC G-protein coupled receptors and thioesterases. The present sequence is  
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
XX CC by them may be used in the prevention, diagnosis and treatment of  
XX CC diseases associated with inappropriate expression of the proteins listed  
XX CC above. Disorders that may be prevented, diagnosed and/or treated include  
XX CC multifactorial diseases with a genetic component, such as autoimmune  
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia),  
XX CC diseases of the nervous system and an infection of pathogenic  
XX CC organisms.  
XX SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other:  
  
Query Match 46.9%; Score 16.4; DB 22; Length 50;  
Best Local Similarity 76.9%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
OY 7 tagaatgggagtggtggtcactcga 32  
||||| ||||| ||||| ||||| |||||  
Db 40 TAGACTGGGGCTCGGCTCGCTCTGAA 15  
  
RESULT 9  
AAF26235/c  
ID AAF26235 standard; DNA: 36 BP.  
XX AC AAF26235;  
XX DT 02-MAY-2001 (first entry)  
XX DE B. megaterium cytochrome P450 monooxygenase BM-3 associated primer B1.  
XX XX  
XX Cytochrome P450 monooxygenase: BM-3; electron donor system; bioreactor;  
XX KM electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase;  
XX KM primer; ss.  
XX OS Bacillus megaterium.  
XX PN WO200107573-A1.  
XX PD 01-FEB-2001.  
XX PF 27-JUL-2000; 2000MO-EP07251.  
XX PR 27-JUL-1999; 99DE-1035115.  
XX PR 10-MAR-2000; 2000DE-1011723.  
XX PA (BADI ) BASF AG.  
XX PI Hauer B, Schmid RD, Schwaneberg U;  
XX DR WPI; 2001-159709/16.  
XX XX

PT	Novel electron donor system useful for the production of
PR	omega-hydroxylated fatty acids comprises an inorganic electron sink and
PI	a mediator which enables the electron transfer -
PS	
XX	Example 2: Page 69; 94pp; German.
CC	This invention describes a novel electron donor system (M1) that
CC	transfers electrons to an enzyme with redox properties comprising an
CC	inorganic, not electrode-bound, electron sink and a mediator which enable
CC	the electron transfer. The invention also describes (1) transferring (M2)
CC	oxygen to a hydrocarbon containing hydrogen donor molecule, where the
CC	hydrogen donor molecule is in a reaction medium comprising the oxygen
CC	transferring enzyme and (M1) in the presence of oxygen and incubating
CC	under suitable reaction conditions; (2) the enzymatic production (M3) of
CC	terminally or subterminally hydroxylated (position omega-1 to omega-4)
CC	fatty acids comprising: (i) mixing a hydroxylatable fatty acid or fatty
CC	acid derivative in the presence of (M1) and cytochrome P450
CC	monooxygenase; and (ii) isolating the hydroxylated product; (3) a
CC	bioreactor useful for the production of omega-hydroxylated fatty acids as
CC	described in (2); and (4) detecting (M4) fatty acid-monooxygenases
CC	comprising: (i) contacting the analyte with a omega-hydroxylatable fatty
CC	acid or a derivative comprising a terminal chromophore or fluorescent
CC	label in (M1); and (ii) qualitatively or quantitatively detecting the
CC	signal. The invention is useful for the production of omega-hydroxylated
CC	fatty acids and the detection of fatty acid monooxygenases. The
CC	invention provides an alternative electron donor system of enzymes with
CC	redox properties that is cheaper and more efficient, where the enzyme
CC	comprises cytochrome 450.
SQ	Sequence 36 BP; 15 A; 6 C; 9 G; 6 T; 0 other;
Query Match	46.3%; Score 16.2; DB 22; Length 36;
Best Local Similarity	72.4%; Pred. No. 1.5e+03;
Matches 21; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
OY	1 catgtctagaatgtagggagtcactct 29
DB	34 CATTTCTTAAATGTCAGGATCCCTCT 6
3ESUJT_10	
AAF26258/C	
ID	AAF26258 standard: DNA: 36 BP.
AC	
AAF26258;	
XX	
02-MAY-2001 (first entry)	
B. megaterium BM-3 associated primer A1.	
Cytochrome P450 monooxygenase: BM-3; electron donor system: bioreactor:	
electron transfer; hydroxylatable fatty acid; fatty acid:monooxygenase;	
primer: ss.	
Bacillus megaterium.	
MO200107573-A1.	
01-FEB-2001.	
27-JUL-2000; 2000WO-EP07251.	
27-JUL-1999; 99DE-1035115.	
10-MAR-2000; 2000DE-1011723.	
(BADI ) BASF AG.	
Hauer B, Schmid RD, Schwaneberg U;	
WPI: 2001-159709/16.	
Novel electron donor system useful for the production of	

[illegible]

PT a mediator which enables the electron transfer -  
XX  
PS  
XX Example 2; Page 75; 94pp; German.  
XX  
CC This invention describes a novel electron donor system (M1) that  
CC transfers electrons to an enzyme with redox properties comprising an  
CC inorganic, not electrode-bound, electron sink and a mediator which enable  
CC the electron transfer. The invention also describes (1) transferring (M2)  
CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the  
CC hydrogen donor molecule is in a reaction medium comprising the oxygen  
CC transferring enzyme and (M1) in the presence of oxygen and incubating  
CC under suitable reaction conditions; (2) the enzymatic production (M3) of  
CC terminally or subterminally hydroxylated (position omega-1 to omega-4)  
CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty  
CC acid derivative in the presence of (M1) and cytochrome P450  
CC monooxygenase; and (11) isolating the hydroxylated product; (3) a  
CC bioreactor useful for the production of omega-hydroxylated fatty acids as  
CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases  
CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty  
CC acid or a derivative comprising a terminal chromophore or fluorescent  
CC label in (M1); and (11) qualitatively or quantitatively detecting the  
CC signal. The invention is useful for the production of omega-hydroxylated  
CC fatty acids and the detection of fatty acid monooxygenases. The  
CC invention provides an alternative electron donor system of enzymes with  
CC redox properties that is cheaper and more efficient, where the enzyme  
CC comprises cytochrome 450.  
XX  
SQ Sequence 36 BP; 15 A; 6 C; 9 G; 6 T; 0 other:  
XX  
Query Match 46.3%; Score 16.2; DB 22; Length 36;  
Best Local Similarity 72.4%; Pred. No. 1.5e+03;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Oy 1 catgtctagaatgggagtggtactct 29  
||| ||| ||| ||| ||| ||| ||| |||  
Db 34 CATTTCTTTAATGTCATGGATCCCTCT 6  
XX  
RESULT 12  
AAF26262/C  
ID AAF26262 standard; DNA; 36 BP.  
XX  
AC AAF26262;  
XX  
DF 02-MAY-2001 (first entry)  
XX  
DE B. megaterium BM-3 associated primer H1.  
XX  
KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;  
KW electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase;  
KW primer; ss.  
XX  
OS Bacillus megaterium.  
XX  
PN WO200107573-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 27-JUL-2000; 2000WO-EP07251.  
XX  
PR 27-JUL-1999; 99DE-1035115.  
PR 10-MAR-2000; 2000DE-1011723.  
XX  
PA (BADT) BASF AG.  
XX  
PI Hauser B, Schmid RD, Schwaneberg U;  
XX  
DR WPI; 2001-159709/16.  
XX  
PT Novel electron donor system useful for the production of  
PT omega-hydroxylated fatty acids comprises an inorganic electron sink and  
PT a mediator which enables the electron transfer -  
XX

XX  
PS  
XX Example 2; Page 76; 94pp; German.  
XX  
CC This invention describes a novel electron donor system (M1) that  
CC transfers electrons to an enzyme with redox properties comprising an  
CC inorganic, not electrode-bound, electron sink and a mediator which enable  
CC the electron transfer. The invention also describes (1) transferring (M2)  
CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the  
CC hydrogen donor molecule is in a reaction medium comprising the oxygen  
CC transferring enzyme and (M1) in the presence of oxygen and incubating  
CC under suitable reaction conditions; (2) the enzymatic production (M3) of  
CC terminally or subterminally hydroxylated (position omega-1 to omega-4)  
CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty  
CC acid derivative in the presence of (M1) and cytochrome P450  
CC monooxygenase; and (11) isolating the hydroxylated product; (3) a  
CC bioreactor useful for the production of omega-hydroxylated fatty acids as  
CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases  
CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty  
CC acid or a derivative comprising a terminal chromophore or fluorescent  
CC label in (M1); and (11) qualitatively or quantitatively detecting the  
CC signal. The invention is useful for the production of omega-hydroxylated  
CC fatty acids and the detection of fatty acid monooxygenases. The  
CC invention provides an alternative electron donor system of enzymes with  
CC redox properties that is cheaper and more efficient, where the enzyme  
CC comprises cytochrome 450.  
XX  
SQ Sequence 36 BP; 15 A; 6 C; 9 G; 6 T; 0 other:  
XX  
Query Match 46.3%; Score 16.2; DB 22; Length 36;  
Best Local Similarity 72.4%; Pred. No. 1.5e+03;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Oy 1 catgtctagaatgggagtggtactct 29  
||| ||| ||| ||| ||| ||| ||| |||  
Db 34 CATTTCTTTAATGTCATGGATCCCTCT 6  
XX  
RESULT 13  
AAF83314  
ID AAF83314 standard; DNA; 36 BP.  
XX  
AC AAF83314;  
XX  
DF 09-JUL-2001 (first entry)  
XX  
DE Human neuropilin-1 (NP-1) DNA amplifying sense primer BUL-265.  
XX  
KW Receptor protein; vascular endothelial growth factor receptor-2; NP-1;  
KW VEGFR-2; neuropilin-1; co-receptor; human; angiogenic; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200131346-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US29579.  
XX  
PR 28-OCT-1999; 99US-0162367.  
XX  
PA (PROCTER & GAMBLE CO.  
XX  
PI Rosenbaum JS, Whitaker GB, Limberg BJ;  
XX  
DR WPI; 2001-308686/32.  
XX  
PT Determining compounds which bind to a complex comprising vascular  
PT endothelial growth factor receptor-2 and Neuropilin-1 to provide  
PT superior pro- and anti-angiogenic agents -  
XX  
PS Example 1; Fig 3; 82pp; English.  
XX



XX Sequence 51 BP; 6 A; 23 C; 16 G; 6 T; 0 other;

Query Match 45.7%; Score 16; DB 22; Length 51;  
 Best Local Similarity 68.8%; Pred. No. 2e+03;  
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 tgctagaatgggagtggtcactctggacc 34  
 |||||  
 Db 10 tgctatgctggygacggygcgcgtcaggtcc 41

Search completed: June 22, 2002, 05:40:15  
 Job time: 5090 sec

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## OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:33:31 ; Search time 98.05 Seconds  
(Without alignments)  
87.682 Million cell updates/sec

Title: US-09-927-267-13

Perfect score: 35

Sequence: 1 catgctagaatggagatgggtcactctgacact 35

## Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 613726

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

## Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/lna/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/lna/backfiles1.seq: \*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.2	52.0	46	6	Patent No. 5196308-1
C 2	17.2	49.1	38	3	US-08-961-083-382
C 3	16.8	48.0	42	1	US-08-086-4288-124
C 4	16.8	48.0	42	2	US-08-468-570-124
C 5	16.8	48.0	42	2	US-08-290-665A-228
C 6	16.8	48.0	42	5	PCT-US95-10398-228
C 7	15.8	45.1	75	1	US-08-482-111-61
C 8	15.4	44.0	81	1	US-08-238-863-78
C 9	15.4	44.0	81	1	US-08-443-407-78
C 10	15.4	44.0	81	5	PCT-US95-05600-222
C 11	15.4	44.0	100	4	US-08-954-395A-28
C 12	15.4	44.0	32	1	US-08-221-817-8
C 13	15.4	42.9	32	1	US-08-454-439-8
C 14	15.4	42.9	32	5	PCT-US94-10487-8
C 15	14.6	41.7	21	1	US-07-665-960A-10
C 16	14.6	41.7	21	2	US-08-106-802-10
C 17	14.6	41.7	21	2	US-08-703-136-10
C 18	14.6	41.7	51	2	US-08-883-795A-10
C 19	14.6	41.7	51	2	US-08-883-795A-26
C 20	14.4	41.1	39	1	US-08-121-202-16
C 21	14.2	40.6	26	4	US-09-268-163-76
C 22	14.2	40.6	33	6	5196305-1
C 23	14.2	40.6	83	4	US-08-729-601A-25
C 24	14.2	40.6	29	2	US-08-664-872-14
C 25	14.2	40.0	29	4	US-09-019-973-16
C 26	14.2	40.0	73	4	US-09-564-805-13
C 27	14.2	40.0	79	1	US-08-384-708A-212

28	14	40.0	79	2	US-08-470-939-10	Sequence 10, App1
29	14	40.0	79	4	US-08-687-421-304	Sequence 304, App
30	14	40.0	79	5	PCT-US96-09452-10	Sequence 10, App1
31	14	40.0	86	1	US-08-447-169A-177	Sequence 177, App
32	14	40.0	96	1	US-08-253-877C-16	Sequence 16, App1
33	14	40.0	96	2	US-08-452-164A-16	Sequence 16, App1
34	14	40.0	96	3	US-08-603-024-15	Sequence 15, App1
35	13.8	39.4	30	2	US-08-829-876-20	Sequence 20, App1
36	13.8	39.4	39	3	US-08-643-704A-37	Sequence 37, App1
37	13.8	39.4	50	1	US-08-171-389-532	Sequence 532, App
38	13.8	39.4	50	1	US-08-123-936-532	Sequence 532, App
39	13.8	39.4	50	2	US-08-475-228A-532	Sequence 532, App
40	13.8	39.4	50	3	US-08-482-080A-532	Sequence 532, App
41	13.8	39.4	50	5	PCT-US93-12388-532	Sequence 532, App
42	13.8	39.4	60	3	US-08-643-704A-11	Sequence 11, App1
43	13.8	39.4	81	1	US-08-238-863-90	Sequence 90, App1
44	13.8	39.4	81	1	US-08-443-407-90	Sequence 90, App1
45	13.8	39.4	81	5	PCT-US95-05600-234	Sequence 234, App1
46	13.6	38.9	100	4	US-08-954-395A-24	Sequence 24, App1
47	13.6	38.9	22	2	US-08-451-822A-6	Sequence 6, App1
48	13.6	38.9	22	4	US-08-323-430-6	Sequence 6, App1
49	13.6	38.9	31	3	US-09-032-894-109	Sequence 109, App
50	13.6	38.9	31	3	US-09-032-894-111	Sequence 111, App
51	13.6	38.9	31	4	US-09-031-626-109	Sequence 109, App
52	13.6	38.9	31	4	US-09-031-626-111	Sequence 111, App
53	13.6	38.9	32	1	US-07-990-965-2	Sequence 2, App1
54	13.6	38.9	40	4	US-09-262-773-128	Sequence 128, App
55	13.6	38.9	42	3	US-08-874-825-42	Sequence 42, App1
56	13.6	38.9	42	3	US-08-663-824-42	Sequence 42, App1
57	13.6	38.9	48	5	PCT-US94-07779-2	Sequence 2, App1
58	13.6	38.9	61	4	US-08-952-793-377	Sequence 377, App
59	13.6	38.9	61	5	PCT-US96-09455A-377	Sequence 377, App
60	13.4	38.3	26	4	US-09-147-915-11	Sequence 11, App1
61	13.4	38.3	28	4	US-09-324-867-42	Sequence 42, App1
62	13.4	38.3	34	3	US-08-814-412-24	Sequence 24, App1
63	13.4	38.3	55	1	US-08-325-253-7	Sequence 7, App1
64	13.2	37.7	20	1	US-08-469-802B-40	Sequence 40, App1
65	13.2	37.7	20	2	US-08-267-803B-58	Sequence 58, App1
66	13.2	37.7	20	4	US-09-178-115-114	Sequence 114, App
67	13.2	37.7	20	4	US-09-177-776-114	Sequence 114, App
68	13.2	37.7	21	2	US-08-845-998-12	Sequence 12, App1
69	13.2	37.7	21	3	US-09-206-537-12	Sequence 12, App1
70	13.2	37.7	21	4	US-09-430-854-12	Sequence 12, App1
71	13.2	37.7	23	1	US-08-683-839B-6	Sequence 6, App1
72	13.2	37.7	25	3	US-08-722-240-27	Sequence 27, App1
73	13.2	37.7	25	3	US-07-601-094-16	Sequence 16, App1
74	13.2	37.7	28	1	US-07-601-094-17	Sequence 17, App1
75	13.2	37.7	28	1	US-08-012-735-16	Sequence 16, App1
76	13.2	37.7	28	1	US-08-012-735-17	Sequence 17, App1
77	13.2	37.7	28	1	US-08-268-799-1	Sequence 1, App1
78	13.2	37.7	28	1	US-08-268-799-7	Sequence 7, App1
79	13.2	37.7	33	5	PCT-US93-01976-4	Sequence 4, App1
80	13.2	37.7	33	5	US-09-277-016-21	Sequence 21, App1
81	13.2	37.7	40	3	US-08-331-394-48	Sequence 48, App1
82	13.2	37.7	41	1	US-08-250-858-48	Sequence 48, App1
83	13.2	37.7	41	1	US-08-446-915-48	Sequence 48, App1
84	13.2	37.7	41	1	US-08-744-139-48	Sequence 48, App1
85	13.2	37.7	41	5	PCT-US95-06639-48	Sequence 48, App1
86	13.2	37.7	42	6	5422260-10	Sequence 48, App1
87	13.2	37.7	42	6	US-08-203-196-3	Sequence 3, App1
88	13.2	37.7	45	5	PCT-US95-01976-3	Sequence 3, App1
89	13.2	37.7	45	5	US-08-171-389-579	Sequence 579, App
90	13.2	37.7	50	1	US-08-171-389-580	Sequence 580, App
91	13.2	37.7	50	1	US-08-133-936-579	Sequence 579, App
92	13.2	37.7	50	1	US-08-133-936-580	Sequence 580, App
93	13.2	37.7	50	1	US-08-475-228A-579	Sequence 579, App
94	13.2	37.7	50	2	US-08-475-228A-580	Sequence 580, App
95	13.2	37.7	50	3	US-08-482-080A-579	Sequence 580, App
96	13.2	37.7	50	3	US-08-482-080A-580	Sequence 580, App
97	13.2	37.7	50	3	PCT-US93-12388-579	Sequence 579, App
98	13.2	37.7	50	5	PCT-US93-12388-580	Sequence 580, App
99	13.2	37.7	50	5	US-08-722-240-16	Sequence 16, App1
100	13.2	37.7	51	3		















C 977 11.4 32.6 23 2 US-08-749-337-19 Sequence 19, Appl  
C 978 11.4 32.6 24 2 US-08-486-839-2 Sequence 2, Appl  
C 979 11.4 32.6 24 2 US-08-854-727-7 Sequence 7, Appl  
C 980 11.4 32.6 24 2 US-08-854-727-27 Sequence 27, Appl  
C 981 11.4 32.6 24 3 US-09-151-011-2 Sequence 2, Appl  
C 982 11.4 32.6 24 4 US-09-038-637-7 Sequence 7, Appl  
C 983 11.4 32.6 24 4 US-09-038-637-39 Sequence 39, Appl  
C 984 11.4 32.6 24 4 US-09-240-918-62 Sequence 62, Appl  
C 985 11.4 32.6 24 4 US-08-968-733-7 Sequence 7, Appl  
C 986 11.4 32.6 24 4 US-08-968-733-39 Sequence 39, Appl  
C 987 11.4 32.6 24 4 US-09-343-623-2 Sequence 2, Appl  
C 988 11.4 32.6 24 5 PCT-US95-11233-7 Sequence 7, Appl  
C 989 11.4 32.6 24 5 PCT-US95-11233-27 Sequence 27, Appl  
C 990 11.4 32.6 25 1 US-08-634-331-11 Sequence 11, Appl  
C 991 11.4 32.6 25 1 US-08-192-946-9 Sequence 9, Appl  
C 992 11.4 32.6 25 5 PCT-US93-08106-2 Sequence 2, Appl  
C 993 11.4 32.6 25 5 PCT-US94-00089-2 Sequence 2, Appl  
C 994 11.4 32.6 26 1 US-08-354-101-5 Sequence 5, Appl  
C 995 11.4 32.6 26 1 US-08-470-834-5 Sequence 5, Appl  
C 996 11.4 32.6 27 1 US-08-591-070A-55 Sequence 55, Appl  
C 997 11.4 32.6 27 1 US-08-474-633A-14 Sequence 14, Appl  
C 998 11.4 32.6 27 2 US-08-480-473B-8 Sequence 8, Appl  
C 999 11.4 32.6 27 2 US-08-927-855-55 Sequence 55, Appl  
C 1000 11.4 32.6 27 3 US-09-257-799-41 Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
5196308-1/c  
; Patent No. 5196308  
; APPLICANT: NEPOM, GERALD T.; NEPOM, BARBARA S.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING THE DOW3.2  
; ALLELE ASSOCIATED WITH INCREASED RISK OF INSULIN-DEPENDENT  
; DIABETES MELLITUS  
; NUMBER OF SEQUENCES: 2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/325,058  
; FILING DATE: 13-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 745,321  
; FILING DATE: 14-JUN-1985  
; SEQ ID NO:1:  
; LENGTH: 46  
; 5196308-1

Query Match 52.0%; Score 18.2; DB 6; Length 46;  
Best Local Similarity 74.2%; Pred. No. 26;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 tgcctagatgggagatgggagctctgac 33  
||| | ||||| | ||||| ||| |  
Db 34 tgcctgagatgggagatgggagctctgac 4

RESULT 2  
US-08-961-083-382/c  
; Sequence 382, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 382:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-083-382

Query Match 49.1%; Score 17.2; DB 3; Length 38;  
Best Local Similarity 73.3%; Pred. No. 67;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 6 ctgaatgggagatgggagctctgac 35  
||||| | ||| | ||| |  
Db 32 ctgaatgggagatgggagctctgac 3

RESULT 3  
US-08-086-428B-124/c  
; Sequence 124, Application US/08086428B  
; Patent No. 5514539  
; GENERAL INFORMATION:  
; APPLICANT: BUKH, J., MILLER, R.H. AND  
; TITLE OF INVENTION: NOCLEOTIDE AND DEDUCED  
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE  
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE  
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN  
; NUMBER OF SEQUENCES: 159  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/086,428B  
; FILING DATE: 29-JUN-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RICHARD W. BORK  
; REGISTRATION NUMBER: 36,459  
; REFERENCE/DOCKET NUMBER: 2026-4070  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; TELEX: 421792



INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-086-428B-124

Query Match 48.0%; Score 16.8; DB 1; Length 42;  
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 7;

OY 1 catgtctagaatgggagatgggtcactc 28  
||||| ||||| || ||||| |||||  
DB 30 CATGTCGAGAAAGCGCTGTGGGACCCCTC 3

RESULT 4  
US-08-468-570-124/C  
Sequence 124, Application US/08468570  
Patent No. 5871962  
GENERAL INFORMATION:  
APPLICANT: BUKH, J., MILLER, R.H. AND  
APPLICANT: PURCELL, R.H.  
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE  
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE  
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN  
NUMBER OF SEQUENCES: 159  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,570  
FILING DATE: 6-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,428  
FILING DATE: 29-JUN-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4070US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-468-570-124

Query Match 48.0%; Score 16.8; DB 2; Length 42;  
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
OY 1 catgtctagaatgggagatgggtcactc 28

DB 30 CATGTCGAGAAAGCGCTGTGGGACCCCTC 3  
||||| ||||| || ||||| |||||

RESULT 5  
US-08-290-665A-228/C  
Sequence 228, Application US/08290665A  
Patent No. 5882852

GENERAL INFORMATION:  
APPLICANT: BUKH, J., MILLER, R.H. AND  
APPLICANT: PURCELL, R.H.  
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND  
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS  
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE  
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES  
NUMBER OF SEQUENCES: 263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,665A  
FILING DATE: 15-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 228:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-290-665A-228

Query Match 48.0%; Score 16.8; DB 2; Length 42;  
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 7;

OY 1 catgtctagaatgggagatgggtcactc 28  
||||| ||||| || ||||| |||||  
DB 30 CATGTCGAGAAAGCGCTGTGGGACCCCTC 3

RESULT 6  
PCT-US95-10398-228/C  
Sequence 228, Application PC/TUS9510398  
GENERAL INFORMATION:  
APPLICANT: BUKH, J., MILLER, R.H. AND  
APPLICANT: PURCELL, R.H.  
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND  
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS  
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE  
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES  
NUMBER OF SEQUENCES: 263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10398  
FILING DATE: 15-AUG-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,428  
FILING DATE: 29 JUNE 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290/665  
FILING DATE: 15 AUGUST 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 228:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-10398-228

Query Match 48.0%; Score 16.8; DB 5; Length 42;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 catgtctagaatgggagtggtcactc 28  
||||| ||| ||| ||| |||

DB 30 CAGTCGAGAAAGCTGTGGGACCTC 3

RESULT 7  
US-08-482-111-61  
Sequence 61, Application US/08482111  
Patent No. 5789539  
GENERAL INFORMATION:  
APPLICANT: Daly, Thomas J.  
APPLICANT: Larosa, Gregory J.  
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of  
NUMBER OF SEQUENCES: 70  
TITLE OF INVENTION: Use  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,111  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 00231/083001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 75 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-111-61

Query Match 45.1%; Score 15.8; DB 1; Length 75;  
Best Local Similarity 65.7%; Pred. No. 3e+02;  
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 catgtctagaatgggagtggtcactcggacct 35  
|| ||| ||| ||| ||| ||| ||| |||

DB 31 CACCTCAGCTGCTGATGTGCTGGGGCTGGACCT 65

RESULT 8  
US-08-238-863-78  
Sequence 78, Application US/08238863  
Patent No. 5503978  
GENERAL INFORMATION:  
APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FEIGON, J.  
TITLE OF INVENTION: HIGH-AFFINITY ssDNA LIGANDS OF HIV-1  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beaton & Swanson, P.C.  
STREET: 4582 South Ulster Street Parkway, Suite  
STREET: #403  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80237  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,863  
FILING DATE: 6-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 850-9900  
TELEFAX: (303) 850-9401  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-238-863-78

Query Match	44.0%;	Score 15.4;	DB 1;	Length 81;
Best Local Similarity	76.0%;	Pred. NO. 4.5e+02;		
Matches 19;	Conservative	0;	Mismatches 6;	Indels 0;
				Gaps 0;

```

Qy      3  tgtctagaatggtgatgggtcact 27
          |||||
Db      35  TGTCTAGAACTTGGAAAGTGTCACT 59

```

RESULT 9  
US-08-443-407-78

```

: Sequence 78, Application US/08443407
: Patent No. 5786462
:
: GENERAL INFORMATION:
:
: APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FELIGON, J
:
: TITLE OF INVENTION: HIGH-AFFINITY ssDNA
: TITLE OF INVENTION: LIGANDS OF HIV-1 REVERSE
: TITLE OF INVENTION: TRANSCRIPTASE
: NUMBER OF SEQUENCES: 94
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/443,407
: FILING DATE:
:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/238,863
: FILING DATE: 6-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/714,131
: FILING DATE: 10-JUNE-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/964,624
: FILING DATE: 21-OCTOBER-1992
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX17/C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
:
: INFORMATION FOR SEQ ID NO: 78:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 81
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-443-407-78

```

Query Match	44.08;	Score 15.4;	DB 1;	length 81;
Best Local Similarity	76.08;	Pred. No. 4.5e+02;		
Matches 19; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY 3 tgtctagaatggygatggygtcact 27  
||||| ||| | |||||  
Db 35 TGTCTAGACTTGGAAAGTGTCACT 59

RESULT 10  
PCT-US95-05600-222

```

Sequence 222, Application PC/TUS9505600
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: NIEDWLANDT, DAN
APPLICANT: WIECKER, MATTHEW
APPLICANT: SCHNEIDER, DANIEL J.
APPLICANT: FEIGON, JULI
APPLICANT: ALLEN, PATRICK
APPLICANT: SULENGER, BRUCE A.
APPLICANT: DOUDNA, JENNIFER, A.
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: Storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238, 863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248, 632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303, 362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361, 795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117, 991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931, 473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964, 624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536, 428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714, 131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536, 428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

```

INFORMATION FOR SEQ ID NO: 222:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-05600-222

Query Match 44.0%; Score 15.4; DB 5; Length 81;  
Best local Similarity 76.0%; Pred. No. 4.5e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 tgcctgaatgggagatgggagct 27  
||||||| ||| | |||||  
Db 35 TGCTGAACTGGAAAGTGTCTACT 59

RESULT 11  
US-08-954-395A-28/C  
Sequence 28, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Sudramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Phillip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Dehlinger & Associates, LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: Frag N4, forward strand  
US-08-954-395A-28

Query Match 44.0%; Score 15.4; DB 4; Length 100;

Best local Similarity 76.0%; Pred. No. 4.7e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 11 atgggagtggtgactctgacct 35  
||||||| | |||||  
Db 96 AAGAGATGGGAATTCGTGACAT 72

RESULT 12  
US-08-221-817-8  
Sequence 8, Application US/08221817  
Patent No. 5532151  
GENERAL INFORMATION:

APPLICANT: Chantry, David  
APPLICANT: Gray, Patrick W.  
APPLICANT: Hoekstra, Merle F.  
TITLE OF INVENTION: A No. 5532151el G Protein-coupled Receptor  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSER: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,817  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/123,932  
FILING DATE: 17 SEP 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5532151and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31981  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-221-817-8

Query Match 42.9%; Score 15; DB 1; Length 32;  
Best local Similarity 78.3%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 atgtcagaatgggagatgggct 24  
||||||| ||| |  
Db 1 ATTTCTAAGATGGGACGTGGCC 23

RESULT 13  
US-08-454-439-8  
Sequence 8, Application US/08454439  
Patent No. 5591618  
GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Gray, Patrick W.



```

; REFERENCE/DOCKET NUMBER: 600.190-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 332-5300
; TELEFAX: (612) 332-9081
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
; ANTI-SENSE: yes
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Oligonucleotide Primer DOB30
; LOCATION: Anneals to codons 97 to 104 of the
; LOCATION: DOB1 transcript of HLA class II
US-07-665-960A-10
    
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Query Match      41.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      11 atgggagatgggtcactctg 31
         |||||  |||||  |||
Db       1 ATGGGAGATGTCACCTGTGG 21
    
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Search completed: June 22, 2002, 05:33:43  
 Job time: 4753 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:59:26 ; Search time 2443.9 Seconds  
(Without alignments) 193.295 Million cell updates/sec

Title: US-09-927-267-13  
Perfect score: 35  
Sequence: 1 catgtctagatcgggagatggggtcactctggacct 35

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
EST: \*  
1: em\_estba: \*  
2: em\_esthm: \*  
3: em\_estin: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pln: \*  
16: em\_gss\_vrc: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	53.1	38	12	A2773847
2	17.4	49.7	79	9	AA668503
3	17.4	49.7	79	9	AA954823
4	17.4	49.7	79	9	AA1082539
5	17.4	49.7	79	9	AA1085281
6	17.4	49.7	79	9	AA142830
7	17.4	49.7	79	9	AA167555
8	17.4	49.7	79	9	AA620456
9	17.4	49.7	85	10	W20254
10	16.6	47.4	60	12	B39007
11	16.6	47.4	100	9	AA429430
12	16.6	46.9	100	9	AA366936
13	16.2	46.3	79	9	AA723716
14	16.2	46.3	81	9	AA166006
15	16.2	45.7	58	9	AA960093
16	16.2	45.7	62	9	AA405653
17	16.2	45.7	79	9	AA107824

18	16	45.7	89	9	AA197197	AM197197 xm38a06.x
19	16	45.7	100	9	AA286603	AA286603 vb78a03.r
20	15.8	45.1	56	12	A2767267	A2767267 IM0566A23
21	15.8	45.1	59	12	BH011505	BH011505 BG02443-5
22	15.8	45.1	81	9	AA775436	AA775436 ad13f09.s
23	15.8	45.1	81	9	AA994005	AA994005 ou42c02.s
24	15.6	44.6	63	12	A2921625	A2921625 1006030G0
25	15.6	44.6	77	10	N44726	N44726 YV37C09.r1
26	15.6	44.6	80	12	A2921665	A2921665 1006031B0
27	15.6	44.6	90	10	BI791330	BI791330 1004f05.Y
28	15.6	44.6	96	10	T97453	T97453 y57h06.r1
29	15.6	44.6	100	9	AA929885	AA929885 vz44d11.r
30	15.4	44.0	40	9	AA921997	AA921997 oma1a10.s
31	15.4	44.0	64	12	HSWC13F04	HSWC13F04 H.sepiens D
32	15.4	44.0	70	9	A1032382	A1032382 ov37e10.x
33	15.4	44.0	70	10	F30991	F30991 HSPD21806.H
34	15.4	44.0	71	10	BI557731	BI557731 603237092
35	15.4	44.0	80	10	BG061881	BG061881 L09525H02-
36	15.4	44.0	81	9	AA464680	AA464680 zx85f06.r
37	15.4	44.0	81	12	A2918804	A2918804 1006008D1
38	15.4	44.0	87	9	A1859974	A1859974 wM22c08.x
39	15.4	44.0	94	9	AA960499	AA960499 vW63e07.s
40	15.4	44.0	100	9	AA907309	AA907309 s155d01.y
41	15.2	43.4	24	12	A2346754	A2346754 IM0082E12
42	15.2	43.4	57	12	B02157	B02157 CSRL-149A11
43	15.2	43.4	79	10	BG272579	BG272579 nah28a06.
44	15.2	43.4	82	10	R06472	R06472 yf09a05.r1
45	15.2	43.4	85	9	AA451958	AA451958 zx12d12.r
46	15.2	43.4	98	12	A2357824	A2357824 IM0099J08
47	15	42.9	49	9	A1383078	A1383078 lc20h09.x
48	15	42.9	50	12	A2794281	A2794281 IM0066C04
49	15	42.9	57	12	A236153	A236153 2M0048J13
50	15	42.9	80	12	TA36H07P	TA36H07P T. brucei
51	15	42.9	86	10	R29008	R29008 F0-76D 22 W
52	15	42.9	89	12	TA36H07Q	TA36H07Q T. brucei
53	15	42.9	93	9	AA692582	AA692582 vc61a08.r
54	15	42.9	96	9	AA090390	AA090390 xc81e12.x
55	15	42.9	99	12	A2512819	A2512819 IM0358I07
56	14.8	42.3	40	9	AA247854	AA247854 2820389.3
57	14.8	42.3	56	10	BI791026	BI791026 1004f05.x
58	14.8	42.3	57	12	A2774746	A2774746 2M0004B04
59	14.8	42.3	60	12	A2759519	A2759519 IM0552G08
60	14.8	42.3	77	10	W58820	W58820 md44b11.r1
61	14.8	42.3	78	9	AT142416	AT142416 q96f1f06.s
62	14.8	42.3	81	9	AA903760	AA903760 OK66e05.s
63	14.8	42.3	83	12	A2381974	A2381974 IM0138F15
64	14.8	42.3	98	9	AT174454	AT174454 an46e03.s
65	14.6	41.7	34	12	AZ818088	AZ818088 2M0087I21
66	14.6	41.7	47	12	A2444521	A2444521 IM0239F13
67	14.6	41.7	52	9	AT397068	AT397068 fb25h05.Y
68	14.6	41.7	52	12	A2843674	A2843674 2M0142G08
69	14.6	41.7	56	9	AT720114	AT720114 as78f06.x
70	14.6	41.7	59	10	T24794	T24794 EST369 Huma
71	14.6	41.7	61	9	AT954288	AT954288 wX59d12.x
72	14.6	41.7	67	9	AA907371	AA907371 OJ70h02.S
73	14.6	41.7	77	12	A2468774	A2468774 IM0281O18
74	14.6	41.7	79	9	AA018118	AA018118 ct91f06.s
75	14.6	41.7	83	9	AA647456	AA647456 vq82d12.s
76	14.6	41.7	87	9	AA243934	AA243934 mx35f08.r
77	14.6	41.7	88	9	AT866758	AT866758 tz25e10.x
78	14.6	41.7	89	9	AT656448	AT656448 ct45h01.x
79	14.6	41.7	91	10	BG142757	BG142757 1689D02.Y
80	14.6	41.7	97	10	BM122580	BM122580 L0512B07-
81	14.4	41.1	43	9	AT283683	AT283683 q172g11.x
82	14.4	41.1	50	9	AT105373	AT105373 AU105373
83	14.4	41.1	55	9	AT1965095	AT1965095 fc86g04.Y
84	14.4	41.1	63	12	A2941669	A2941669 2M0201F04
85	14.4	41.1	67	9	AT791108	AT791108 uk55g10.Y
86	14.4	41.1	67	9	AA161388	AA161388 zq39f12.s
87	14.4	41.1	70	9	AT969965	AT969965 wq78e01.x
88	14.4	41.1	79	10	H53571	H53571 CHR220310.C
89	14.4	41.1	82	9	AF211796	AF211796 AF211796
90	14.4	41.1	82	12	A2443108	A2443108 IM0237F07





237	13.4	38.3	55	12	TA121A10P	AL465712 T. brucei	c 310	13.2	37.7	69	9	AI588687
238	13.4	38.3	58	10	R76020	R76020 y122g10.s1	c 311	13.2	37.7	70	9	AA460112
239	13.4	38.3	61	9	AI735643	AI735643 at19a05.x	c 312	13.2	37.7	71	12	AZ816914
240	13.4	38.3	63	10	B1048110	B1048110 B1048110	c 313	13.2	37.7	71	12	TA9C01P
241	13.4	38.3	65	9	AM695641	AM695641 NP097C06S	c 314	13.2	37.7	73	10	BF400540
242	13.4	38.3	65	12	BH415614	BH415614 1007043HO	c 315	13.2	37.7	73	12	AZ919172
243	13.4	38.3	67	10	R71808	R71808 yJ86b01.r1	c 316	13.2	37.7	75	9	AA606357
244	13.4	38.3	69	12	CNS02XR5	AL128714 Telradon	c 317	13.2	37.7	76	10	D43333
245	13.4	38.3	71	9	AA966926	AA966926 ua38a07.r	c 318	13.2	37.7	78	9	AA746106
246	13.4	38.3	71	10	B1557812	B1557812 603236992	c 319	13.2	37.7	78	10	D82266
247	13.4	38.3	72	10	U44175	U44175 EN044175 AS	c 320	13.2	37.7	81	9	AV565298
248	13.4	38.3	72	10	BF021521	BF021521 uy48b10.y	c 321	13.2	37.7	83	9	AA921081
249	13.4	38.3	72	10	BF031325	BF031325 601454547	c 322	13.2	37.7	84	9	AI725315
250	13.4	38.3	73	9	AA976253	AA976253 oc03f04.s	c 323	13.2	37.7	84	10	BG169944
251	13.4	38.3	73	9	AI160767	AI160767 qb53f06.x	c 324	13.2	37.7	85	9	AA810795
252	13.4	38.3	74	12	AZ330761	AZ330761 1M0056L10	c 325	13.2	37.7	85	9	AI477019
253	13.4	38.3	76	9	AI182038	AI182038 ud73c07.y	c 326	13.2	37.7	85	10	BG815145
254	13.4	38.3	77	9	AI655605	AI655605 ts99c07.x	c 327	13.2	37.7	86	9	AA666896
255	13.4	38.3	77	12	AZ483071	AZ483071 1M0308F05	c 328	13.2	37.7	87	12	AZ8383619
256	13.4	38.3	78	12	AZ513591	AZ513591 1M0359D11	c 329	13.2	37.7	87	12	AZ807295
257	13.4	38.3	79	9	AA764740	AA764740 n263d05.s	c 330	13.2	37.7	88	12	AZ438919
258	13.4	38.3	79	9	AA421588	AA421588 z225e02.r	c 331	13.2	37.7	89	9	AI493950
259	13.4	38.3	79	10	BF140210	BF140210 601786792	c 332	13.2	37.7	89	10	BI192026
260	13.4	38.3	79	10	BF147359	BF147359 US30e02.x	c 333	13.2	37.7	91	9	AI331553
261	13.4	38.3	80	12	AZ417201	AZ417201 1M0192H16	c 334	13.2	37.7	91	10	R50465
262	13.4	38.3	81	12	AZ508498	AZ508498 1M0350J24	c 335	13.2	37.7	93	12	AZ805947
263	13.4	38.3	82	9	AA676707	AA676707 z364d04.s	c 336	13.2	37.7	93	12	AZ872079
264	13.4	38.3	83	9	AA429536	AA429536 zw74c11.r	c 337	13.2	37.7	93	12	BH227263
265	13.4	38.3	83	12	AZ580213	AZ580213 1M0368C21	c 338	13.2	37.7	94	9	AI2343604
266	13.4	38.3	83	12	AZ774496	AZ774496 2M0040G02	c 339	13.2	37.7	94	9	AA074184
267	13.4	38.3	85	9	BE223013	BE223013 hu46a04.x	c 340	13.2	37.7	95	12	AZ648429
268	13.4	38.3	85	12	AZ774997	AZ774997 2M0004G24	c 341	13.2	37.7	97	10	R60419
269	13.4	38.3	87	12	AZ807295	AZ807295 2M0070K01	c 342	13.2	37.7	98	12	AZ165956
270	13.4	38.3	88	9	AV837986	AV837986 AV837986	c 343	13.2	37.7	99	9	AI006397
271	13.4	38.3	88	10	B1029074	B1029074 B1029074	c 344	13.2	37.7	99	9	AM059901
272	13.4	38.3	88	12	AF219064	AF219064 AF219064	c 345	13.2	37.7	100	9	AM620205
273	13.4	38.3	89	10	N20346	N20346 yx38f01.s1	c 346	13.2	37.7	100	10	BF801248
274	13.4	38.3	90	9	AA923319	AA923319 o144b05.s	c 347	13.2	37.7	100	10	BF539034
275	13.4	38.3	90	10	BG405953	BG405953 s8c40b04.	c 348	13.2	37.7	100	12	AZ456564
276	13.4	38.3	91	9	AI196205	AI196205 u170c05.y	c 349	13.2	37.7	100	12	AZ784820
277	13.4	38.3	91	10	T64061	T64061 yC05c10.r1	c 350	13.2	37.7	100	12	AZ784820
278	13.4	38.3	91	10	BE334223	BE334223 US30e02.y	c 351	13.2	37.7	100	12	BE336410
279	13.4	38.3	92	10	HS011941	HS011941 Homo sapi	c 352	13.2	37.7	100	10	BF801248
280	13.4	38.3	92	10	HS5123	HS5123 CHR220062.C	c 353	13.2	37.7	100	10	BF539034
281	13.4	38.3	94	12	BH223219	BH223219 1006106E1	c 354	13.2	37.7	100	12	AZ456564
282	13.4	38.3	95	9	AA681827	AA681827 vu75a01.r	c 355	13.2	37.7	100	12	AZ784820
283	13.4	38.3	95	9	AA930834	AA930834 my55e05.r	c 356	13.2	37.7	100	12	AZ784820
284	13.4	38.3	95	10	BG076487	BG076487 H3003B06-	c 357	13.2	37.7	100	12	BE336410
285	13.4	38.3	95	12	AZ514788	AZ514788 1M0361A17	c 358	13.2	37.7	100	10	BF801248
286	13.4	38.3	96	12	AZ423192	AZ423192 1M0202M07	c 359	13.2	37.7	100	10	BF539034
287	13.4	38.3	97	10	T81216	T81216 yd96g08.r1	c 360	13.2	37.7	100	12	AZ456564
288	13.4	38.3	98	10	H59870	H59870 yrl13h05.s1	c 361	13.2	37.7	100	12	AZ784820
289	13.4	38.3	100	9	AL649251	AL649251 AL649251	c 362	13.2	37.7	100	12	AZ784820
290	13.4	38.3	100	9	AM370035	AM370035 RC6-BT024	c 363	13.2	37.7	100	12	BE336410
291	13.4	38.3	100	10	BG910769	BG910769 602810458	c 364	13.2	37.7	100	10	BF801248
292	13.2	37.7	100	12	AZ817178	AZ817178 2M0086C21	c 365	13.2	37.7	100	10	BF539034
293	13.2	37.7	46	9	AA796136	AA796136 vp18a03.r	c 366	13.2	37.7	100	12	AZ456564
294	13.2	37.7	49	9	AI269199	AI269199 qf68f01.x	c 367	13.2	37.7	100	12	AZ784820
295	13.2	37.7	50	9	AI819158	AI819158 wj94c07.x	c 368	13.2	37.7	100	12	AZ784820
296	13.2	37.7	50	9	AI010680	AI010680 AI010680	c 369	13.2	37.7	100	12	AZ784820
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307	13.2	37.7	65	12	BH218101	BH218101 1006074F1	c 380	13.2	37.7	100	12	AZ784820
308	13.2	37.7	67	9	AI901117	AI901117 sc19h05.y	c 381	13.2	37.7	100	12	AZ784820
309	13.2	37.7	67	10	H39403	H39403 DR95 IFNGm	c 382	13.2	37.7	100	12	AZ784820

C 383	13	37.1	76	9	A1748627	C 456	12.8	36.6	67	12	A2508991	A2508991	1M0351A14
C 384	13	37.1	77	12	A2633034	457	12.8	36.6	67	12	TAl62F060	TA162F060	TA162F060
C 385	13	37.1	78	12	A2801938	458	12.8	36.6	68	12	A2822259	A2822259	A2822259
C 386	13	37.1	79	12	A2918536	C 459	12.8	36.6	73	10	F28512	F28512	F28512
C 387	13	37.1	79	9	AA886266	460	12.8	36.6	74	10	D21007	D21007	D21007
C 388	13	37.1	79	9	AA190950	461	12.8	36.6	75	9	AA144884	AA144884	AA144884
C 389	13	37.1	81	9	AU055641	C 462	12.8	36.6	75	10	BI916780	BI916780	BI916780
C 390	13	37.1	82	9	AA913406	463	12.8	36.6	75	10	H41220	H41220	H41220
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C 392	13	37.1	82	9	AA987833	C 465	12.8	36.6	78	9	AA436198	AA436198	AA436198
C 393	13	37.1	83	12	A2784268	466	12.8	36.6	80	10	BI173107	BI173107	BI173107
C 394	13	37.1	83	12	A2514475	467	12.8	36.6	81	12	BH624425	BH624425	BH624425
C 395	13	37.1	83	12	BH224287	C 468	12.8	36.6	82	9	AA813666	AA813666	AA813666
C 396	13	37.1	84	9	AA272792	469	12.8	36.6	82	9	AL653374	AL653374	AL653374
C 397	13	37.1	84	12	A2609829	C 470	12.8	36.6	83	9	A1624949	A1624949	A1624949
C 398	13	37.1	85	9	AA124662	471	12.8	36.6	83	12	A2514421	A2514421	A2514421
C 399	13	37.1	85	9	AA194691	472	12.8	36.6	83	12	A2953673	A2953673	A2953673
C 400	13	37.1	86	10	BI324530	473	12.8	36.6	84	9	AT458933	AT458933	AT458933
C 401	13	37.1	86	10	T11175	474	12.8	36.6	84	10	R05954	R05954	R05954
C 402	13	37.1	88	9	AA302701	475	12.8	36.6	85	12	A2485432	A2485432	A2485432
C 403	13	37.1	88	10	N29378	C 476	12.8	36.6	86	9	AA253794	AA253794	AA253794
C 404	13	37.1	89	9	AA194799	477	12.8	36.6	86	10	BM052185	BM052185	BM052185
C 405	13	37.1	90	9	AI654260	478	12.8	36.6	86	10	BM052185	BM052185	BM052185
C 406	13	37.1	93	10	R39462	C 479	12.8	36.6	86	12	A2763222	A2763222	A2763222
C 407	13	37.1	94	10	WB8037	480	12.8	36.6	86	12	CNS03709	CNS03709	CNS03709
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C 412	13	37.1	97	9	AA580891	485	12.8	36.6	89	10	W12556	W12556	W12556
C 413	13	37.1	97	10	BJ034034	486	12.8	36.6	89	12	AZ403820	AZ403820	AZ403820
C 414	13	37.1	97	12	A2513981	487	12.8	36.6	91	9	AT126208	AT126208	AT126208
C 415	13	37.1	97	12	B33978	488	12.8	36.6	91	9	BI931845	BI931845	BI931845
C 416	13	37.1	98	9	AF211614	C 489	12.8	36.6	91	10	BF578422	BF578422	BF578422
C 417	13	37.1	98	9	AI973787	490	12.8	36.6	91	12	BH218633	BH218633	BH218633
C 418	13	37.1	98	10	T25794	C 491	12.8	36.6	92	12	A2310944	A2310944	A2310944
C 419	13	37.1	98	12	BE718537	492	12.8	36.6	94	12	A299806	A299806	A299806
C 420	13	37.1	98	12	CNS04PYV	C 493	12.8	36.6	94	9	AA444177	AA444177	AA444177
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C 422	13	37.1	99	10	BE718390	495	12.8	36.6	95	9	AV914458	AV914458	AV914458
C 423	13	37.1	100	9	AA279164	496	12.8	36.6	95	12	A2437964	A2437964	A2437964
C 424	13	37.1	100	9	AAW389472	C 497	12.8	36.6	95	12	A2633214	A2633214	A2633214
C 425	13	37.1	100	9	AA428424	498	12.8	36.6	95	12	BH222731	BH222731	BH222731
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C 429	13	37.1	100	12	BH612928	502	12.8	36.6	97	9	AA897326	AA897326	AA897326
C 430	12.8	36.6	21	12	A2801236	503	12.8	36.6	97	9	AI950903	AI950903	AI950903
C 431	12.8	36.6	27	12	A2997581	C 504	12.8	36.6	97	9	AA198324	AA198324	AA198324
C 432	12.8	36.6	29	12	AG019559	505	12.8	36.6	97	9	AA617925	AA617925	AA617925
C 433	12.8	36.6	35	12	TA386F0Q	C 506	12.8	36.6	97	12	A2457629	A2457629	A2457629
C 434	12.8	36.6	37	9	AA906610	507	12.8	36.6	97	12	A2978575	A2978575	A2978575
C 435	12.8	36.6	37	9	AI302081	C 508	12.8	36.6	98	9	AA795589	AA795589	AA795589
C 436	12.8	36.6	37	12	A2760974	C 509	12.8	36.6	99	9	AT087352	AT087352	AT087352
C 437	12.8	36.6	37	12	A2760974	510	12.8	36.6	99	9	AU009022	AU009022	AU009022
C 438	12.8	36.6	40	10	H30578	511	12.8	36.6	99	9	AU009026	AU009026	AU009026
C 439	12.8	36.6	41	10	BI196943	C 512	12.8	36.6	99	9	AU076744	AU076744	AU076744
C 440	12.8	36.6	48	12	A2777027	513	12.8	36.6	99	9	AA494151	AA494151	AA494151
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C 445	12.8	36.6	53	9	AI906692	518	12.8	36.6	100	9	AA896835	AA896835	AA896835
C 446	12.8	36.6	55	9	AI736052	519	12.8	36.6	100	9	AA9598030	AA9598030	AA9598030
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C 448	12.8	36.6	60	9	AA426872	521	12.8	36.6	100	10	BG277705	BG277705	BG277705
C 449	12.8	36.6	60	10	C00950	C 522	12.8	36.6	100	10	BG330231	BG330231	BG330231
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C 451	12.8	36.6	61	9	AA293064	524	12.8	36.6	100	10	BE667590	BE667590	BE667590
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## ALIGNMENTS

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RESULT 1
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DEFINITION 2M000109R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ773847
VERSION AZ773847.1 GI:12898643
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

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REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
and Wright,D., Weiss,R., Stokes,R., Tinney,A., von Niederhausen,A.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: F column: 09
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Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers

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## FEATURES

## source

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/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0001F09"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g147321141g1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 12 a 6 c 10 g 10 t
ORIGIN
Query Match 53.1%; Score 18.6; DB 12; Length 38;
Best Local Similarity 84.0%; Pred. No. 3.4e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 catgtctagaatgggagatggatgctca 25
Db 14 CATGCTAGAGTGGGATGGATGTAACA 38
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DEFINITION ab86h11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone
IMAGE:853893 3' similar to TR:G1336628 G1336628 EGF REPEAT
TRANSMEMBRANE PROTEIN. ;, mRNA sequence.
ACCESSION AA668503
VERSION AA668503.1 GI:2630002
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 79)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Stepcoe,M., Tan,F., Theisling,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

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## FEATURES

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	BASE COUNT	29 a 19 c 17 g 14 t
	ORIGIN	
	Query Match	49.7%; Score 17.4; DB 9; Length 79;
	Best Local Similarity	68.6%; Pred. No. 1.le+04;
	Matches	24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Oy	1 catgtctagaattgggagtgcactcttgacct 35 	
Db	50 CTTGTCTGAATGCAGTGTTGTCTCGTCTCAGCT 16	
RESULT 3		
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LOCUS	AA954823	
DEFINITION	0099d08..s1 NCI-CGAP Kid6 Homo sapiens CDNA clone IMAGE:1574319 3'	
	similar to TR:061204 061204 EGF REPEAT TRANSMEMBRANE PROTEIN.	
	:contains Alu repetitive element;; mRNA sequence.	
ACCESSION	AA954823	
VERSION	AA954823.1 GI:3118518	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 79) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)	
JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmerit-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: www-bio.llnl.gov/dbirp/image/image.html Insert length: 549 Std Error: 0.00 Seq primer: -40ml3 fwd. RT from Amersham High quality sequence stop: 1.	
FEATURES	Location/Qualifiers	
Source	1..79 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1574319" /clone_lib="NCI-CGAP_Kid6" /sex="mixed" /tissue_type="kidney tumor" /lab_host="SOLR (kanamycin resistant)" /note="Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt, Pooled kidney tumors, 5' adaptor sequence: 5' GAATTCGGACGAG 3' 3' adaptor sequence: 5' CTCGACTTTT TTTT TTTT TTTT 3'"	
BASE COUNT	26 a 19 c 16 g 15 t	3 others
ORIGIN		

Query Match	49.7%;	Score 17.4;	DB 9;	Length 79;
Best Local Similarity	68.6%;	Pred. No. 1.1e+04;		
Matches	24;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;
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	50	CTTGTTCGAATGCTGTTGTGTCTCAGTCGTGCAGGCT 16		
RESULT 4				
AI082539/c				
DEFINITION	AI082539	79 bp	mrna	linear EST 13-AUG-1998
	ox55f04.s1 Soares total_fetus.NB2HF8.9w Homo sapiens CDNA clone			
	IMAGE:1660255.3, similar to TR:Q61204 Q61204 EGF REPEAT			
	TRANSMEMBRANE PROTEIN. ;, mRNA sequence.			
ACCESSION	AI082539			
VERSION	AI082539.1	GI:3419331		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 79)			
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index			
COMMENT	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	This clone is available royalty-free through LNL; contact the			
	IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information.			
	Trace considered overall poor quality			
	Seq primer: -40m13 fwd. ER from Amersham			
	High quality sequence stop: 1.			
FEATURES	Location/Qualifiers			
source	1..79			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:1660255"			
	/clone_lib="Soares-total_fetus_NB2HF8_9w"			
	/dev_stage="8-9 weeks"			
	/lab_host="DH10B"			
	/note="Vector: pT7T3D-Pac (Pharmacia) with a modified			
	polylinker; site.1: Not I; site.2: Eco RI; 1st strand cDNA			
	was prepared from mRNA obtained from pooled 8-9 week			
	(total) fetus material with a Not I - oligo(dT) primer [5'			
	TGTTACCAATCTGCAATGAGCGGCGCCGCTTAATTTTTTTTTTTT 3'].			
	Double-stranded cDNA was ligated to Eco RI adaptors			
	(Pharmacia), digested with Not I and cloned into the Not I			
	and Eco RI sites of the modified pT7T3 vector. Library			
	went through one round of normalization, and was			
	constructed by Bento Soares and M. Fatima Bonaldo. "			
BASE COUNT	29 a	19 c	17 g	14 t
ORIGIN				
Query Match	49.7%;	Score 17.4;	DB 9;	Length 79;
Best Local Similarity	68.6%;	Pred. No. 1.1e+04;		
Matches	24;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;
Db	1	catgctagaatcgggagatcggtcactctgagacct 35		
	50	CTTGTTCGAATGCTGTTGTGTCTCAGTCGTGCAGGCT 16		
RESULT 5				
AI085281/c				
DEFINITION	AI085281	79 bp	mrna	linear EST 17-AUG-1998
	qf18e06.x1 NCI CGAP Brn25 Homo sapiens CDNA clone IMAGE:1750402 3'			
	similar to TR:Q61204 Q61204 EGF REPEAT TRANSMEMBRANE PROTEIN. ;,			
	mrna sequence.			
ACCESSION	AI085281			



VERSION	AI085281.1	GI:3423704
KEYWORDS	ESF.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/nclogap.	
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAAP), Tumor Gene Index	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.	
FEATURES	cdna library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cdna library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	
SOURCE	Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amer sham High quality sequence stop: 1. Location/Qualifiers 1..79 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1750402" /clone_1lb="NCI-CGAP_Brn25" /tissue_type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cdna was primed with a Not I - oligo(dT) primer [5' TGGTACCAATCTGAAAGTGGAGCGCGCATAGGTTTGTGTTTTTTTTTTTTTTT 3']; double-stranded cdna was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	30 a 17 c 16 g 16 t	
ORIGIN		
Query Match	49.7%; Score 17.4; DB 9; Length 79;	
Best Local Similarity	68.6%; Pred. No. 1.le04;	
Matches 24; Conservative	0; Mismatches 11; Indels 0; Gaps 0;	
Q1	1 catgctagatggagatcggtgctcctcgacct 35	
Q2	1	
Q3	50 CTTGTCGATGGCTTGTCTCAGTCTGCACT 16	
RESULT	6	
AA142830/c		
LOCUS	79 bp mRNA linear EST 04-DEC-1996	
DEFINITION	Z140B01.s1 Soares-Pregnant-uterus_NBHPU Homo sapiens CDNA clone	
IMAGE:504361 3'	similar to TR:G1336528 G1336528 Esf REPEAT	
TRANSMEMBRANE PROTEIN ;	mRNA sequence.	
ACCESSION	AA142830	
VERSION	AA142830.1	
KEYWORDS	GI:1712235	
SOURCE	EST.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maitra, M., Parsons, J.,	

TITLE	Ritkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 1. Location/Qualifiers 1. 79 /organism="Homo sapiens" /db_xref="GDB:3809349" /db_xref="taxon:9606" /clone="IMAGE:504361" /clone_lib="Soares_pregnant_uterus_NBHPU" /sex="Female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: uterus; Vector: pT73-Pac; Site: 1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACGGAAGAAATTCGCGCGCCCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."		
FEATURES	source		
BASE COUNT	29 a 19 c 17 g 14 t		
ORIGIN			
Query Match	49.7%; Score 17.4; DB 9; Length 79;		
Best Local Similarity	68.6%; Pred. No. 1.1e+04;		
Matches	24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
Db	1 catgctagaatgggagtgagtcacctgagcct 35 1 111 111111 1 1111111 11 D0 50 CTTGTTTGAAATGGTGTGTCAGTCTCGAGCT 16		
RESULT 7			
LOCUS	AI675555 79 bp mRNA linear EST 17-DEC-1999		
DEFINITION	wC01h12.x1 NCI-CGAP Pr28 Homo sapiens cDNA clone IMAGE:2313959 3'		
ACCESSION	AI675555		
VERSION	AI675555.1 GI:4876035		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 79)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-rt@mail.nih.gov Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be		



found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1165 Std Error: 0.00  
Seq primer: -400P from Gldco  
High quality sequence stop: 1.

## FEATURES

## SOURCE

1..79

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_id="IMAGE:2313959"

/clone\_lib="NCI\_CGAP\_P128"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI\_CGAP\_P122 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
985608-986759, 1101192-1101959, and 121928-1220615)."  
Subtraction by Bento Soares and M. Fatima Bonaudo.

## BASE COUNT

29 a 20 c 16 g 14 t

## ORIGIN

## Query Match

Best Local Similarity 49.7%; Score 17.4; DB 9; Length 79;  
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 catgctagaatggatgggctccttgacct 35

Db 50 CTGTTCTGAATGGTGTGTGTCAGTGCACACT 16

RESULT 8 79 bp mRNA linear EST 09-MAR-1998  
AA620456  
LOCUS a658d08.s1 StrataGene lung carcinoma 937218 Homo sapiens cDNA clone  
DEFINITION IMAGE:951087 3' similar to TR:G1336628 G1336628 BGF REPEAT  
TRANSMEMBRANE PROTEIN.; mRNA sequence.

ACCESSION AA620456  
VERSION AA620456.1 GI:2524395  
KEYWORDS EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 79)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
, J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theisling, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.

## TITLE

Mashtu-NCI human EST Project

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 587 Std Error: 0.00  
Seq primer: -40m13 fwd. 5' from Amersham  
High quality sequence stop: 1.

## FEATURES

## SOURCE

1..79

/organism="Homo sapiens"

/db\_xref="taxon:9606"

## BASE COUNT

29 a 19 c 17 g 14 t

## ORIGIN

Query Match 49.7%; Score 17.4; DB 9; Length 79;  
Best Local Similarity 68.6%; Pred. No. 1.1e+04;  
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 catgctagaatggatgggctccttgacct 35

Db 50 CTGTTCTGAATGGTGTGTGTCAGTGCACACT 16

RESULT 9 85 bp mRNA linear EST 03-MAY-1996  
W20254  
LOCUS z042a10.r1 Soares-parathyroid.tumor.NbHPA Homo sapiens cDNA clone  
DEFINITION IMAGE:306234 5' similar to WP:145E12.1 CE02737.; mRNA sequence.

ACCESSION W20254  
VERSION W20254.1 GI:1296143  
KEYWORDS EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 85)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston  
, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The Mashtu-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: mob.REGA+ER

High quality sequence stop: 1.

## FEATURES

## SOURCE

1..85

/organism="Homo sapiens"

/db\_xref="GDB:1249644"

/db\_xref="taxon:9606"

/clone\_id="IMAGE:306234"

/clone\_lib="Soares-parathyroid.tumor.NbHPA"

/tissue\_type="parathyroid tumor"

/dev\_stage="adult"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: parathyroid gland; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo (dt)  
primer

[5'-TGTTACCAATCTGAAGTGGAGGCGCCGACCAATTTTTTTTTTTTTTTTTT  
TTTTT-3'], double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and



Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL0&t2=IL0-HT0156-  
251099-132-a03&t3=1999-10-25&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 38  
High quality sequence stop: 100.

## FEATURES

Location/Qualifiers  
1..100/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="HT0156"  
/dev\_stage="Adult"/note="Organ: head/neck; Vector: puc18; Site:1: SmaI;  
Site:2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."BASE COUNT  
20 a 22 c 30 g 28 t

## ORIGIN

Query Match 46.9%; Score 16.4; DB 9; Length 100;  
Best Local Similarity 76.9%; Pred. NO. 2.6e+04;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;Oy 5 tctagaatgggagatggggtcactctg 30  
||| ||| ||| ||| ||| ||| ||| |||  
Db 41 TCAGAGAGGAGATGTCGTCATGTG 66RESULT 13  
AA723716/c 79 bp mRNA linear EST 29-DEC-1998  
LOCUS  
DEFINITION AB85f03.s1 Soares\_NFL.T.GBC.SI Homo sapiens cDNA clone  
IMAGE:1325885.3' similar to TR:008567 008567 GUG-DOMAIN PROTEIN  
HOMER,, mRNA sequence.ACCESSION  
AA723716  
AA723716.1 GI:2741423VERSION  
KEYWORDS  
SOURCE

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 79)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENTUnpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.govThis clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert Length: 482 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.

## FEATURES

Location/Qualifiers  
1..79/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1325885"/clone\_id="Soares\_NFL.T.GBC.SI"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pF73D-Pac (Pharmacia) with  
a modified polylinker; Site:1: Not I; Site:2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL9W, testis NHT, and B-cell  
NCL-CGAP-GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

## BASE COUNT

20 a 28 c 20 g 11 t

## ORIGIN

Query Match 46.3%; Score 16.2; DB 9; Length 79;  
Best Local Similarity 85.7%; Pred. NO. 3e+04;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;Oy 12 tggggatggggtcactctgga 32  
||| | ||| ||| ||| ||| ||| |||  
Db 50 TGGTGTGGGCGTCATCTCGA 30RESULT 14  
AA166006/c 81 bp mRNA linear EST 12-FEB-1997  
LOCUS  
DEFINITION ms24d02.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone  
IMAGE:607875.5' similar to gb:U09189 Mus musculus lorixin gene,  
complete cds (MOUSE),, mRNA sequence.ACCESSION  
AA166006  
AA166006.1 GI:1744553VERSION  
KEYWORDS  
SOURCE

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 81)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisels,S., Kucab,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.TITLE  
JOURNAL  
COMMENTThe WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST ProjectWashington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:373307  
Seq primer: -28m13 rev1 ET from Amersham.

## FEATURES

Location/Qualifiers  
1..81/organism="Mus musculus"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:607875"  
/clone\_id="Stratagene mouse skin (#937313)"  
/sex="females"  
/tissue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site:1: EcoRI  
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT. Whole skin from 11 week old C57BL/6 female mice.

Query Match 46.3%; Score 16.2; DB 9; Length 81;  
 Best Local Similarity 72.4%; Pred. No. 3e+04;  
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 57 CTGAAATGGAGGTAGTCATTCAGAAAC 29

## RESULT 15

AA960093

LOCUS ub54a10.s1 Soares-mammary-gland\_NMLMG Mus musculus cDNA clone  
 DEFINITION IMAGE:1381530 3' similar to TR:P70441 P70441 PROTEIN CO-FACTOR. ;,  
 mRNA sequence.

ACCESSION

AA960093.1 GI:3125993

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 58)  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

The WashU-HMI Mouse EST Project  
 Unpublished (1996)

JOURNAL

COMMENT

Contact: Maria M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:903998

Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Possible reversed clone: polyT not found  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.

FEATURES

Source

1.58

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:1381530"

/clone\_1lb="Soares.mammary-gland\_NMLMG"

/sex="female (lactating)"

/tissue\_type="mammary gland"

/lab\_host="DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from mammary  
 gland tissue from a lactating female, and was then primed  
 with a Not I - oligo(dT) primer. Double-stranded cDNA was  
 ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified p773 vector. Library is normalized. Library  
 was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 45.7%; Score 16; DB 9; Length 58;  
 Best Local Similarity 68.8%; Pred. No. 3.4e+04;  
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 21 AAGCCCGAATGGGTATGCTTCAACCTGCAC 52

Search completed: June 22, 2002, 05:00:13  
 Job time: 3273 sec

BASE COUNT  
 ORIGIN

15 a 16 c 18 g 9 t



**THIS PAGE BLANK (uspto)**

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:07:20 ; Search time 1963.49 Seconds  
(without alignments)  
383.682 Million cell updates/sec

Title: US-09-927-267-12

Perfect score: 36

Sequence: 1 gcgaagctccacatgagccagacccaagt 36

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 843946

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : GenEmbl1.\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_pro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
73	16	44.4	16	16	AX299123 Sequence
72	16	44.4	16	16	AR091831 Sequence
71	16	44.4	16	16	AR157733 Sequence
70	16	44.4	16	16	AR171488 Sequence
69	16	44.4	16	16	BD005508 Compositi
68	16	44.4	16	16	AX326742 Sequence
67	16	44.4	16	16	AX275053 Sequence
66	16	44.4	16	16	AX63737 Sequence 1
65	16	44.4	16	16	AX36805 Sequence 24
64	16	44.4	16	16	AR075883 Sequence
63	16	44.4	16	16	AR097672 Sequence
62	16	44.4	16	16	AX277694 Sequence
61	16	44.4	16	16	AF166785 Hepatitis
60	16	44.4	16	16	AF166788 Hepatitis
59	16	44.4	16	16	AF166792 Hepatitis
58	16	44.4	16	16	AF166801 Hepatitis
57	16	44.4	16	16	A09021 Oligonucleo
56	16	44.4	16	16	A09020 Oligonucleo
55	16	44.4	16	16	AX248413 Sequence
54	16	44.4	16	16	I15069 Sequence 25
53	16	44.4	16	16	I17143 Sequence 25
52	16	44.4	16	16	AR140869 Sequence
51	16	44.4	16	16	AR150819 Sequence
50	16	44.4	16	16	I65697 Sequence 57
49	16	44.4	16	16	I67929 Sequence 57
48	16	44.4	16	16	I90150 Sequence 57
47	16	44.4	16	16	AX076524 Sequence
46	16	44.4	16	16	AR080275 Sequence
45	16	44.4	16	16	AF166789 Hepatitis
44	16	44.4	16	16	AX339342 Sequence
43	16	44.4	16	16	AX157642 Sequence
42	16	44.4	16	16	AX162831 Sequence
41	16	44.4	16	16	AX162832 Sequence
40	16	44.4	16	16	AR024281 Sequence
39	16	44.4	16	16	AR045134 Sequence
38	16	44.4	16	16	BD011358 Chimeric
37	16	44.4	16	16	E43828 Chimeric an
36	16	44.4	16	16	A52096 Sequence 6
35	16	44.4	16	16	J02568 Influenza A
34	16	44.4	16	16	286021 M.musculus
33	16	44.4	16	16	286019 M.musculus
32	16	44.4	16	16	A23760 TGF-beta hy
31	16	44.4	16	16	A50804 Sequence 25
30	16	44.4	16	16	AR109995 Sequence
29	16	44.4	16	16	AR069550 Sequence
28	16	44.4	16	16	AR069551 Sequence
27	16	44.4	16	16	A09018 Oligonucleo
26	16	44.4	16	16	S48391 Col12A1-alp
25	16	44.4	16	16	A27931 Chimeric VI
24	16	44.4	16	16	A27947 Oligonucleo
23	16	44.4	16	16	I26284 Sequence 33
22	16	44.4	16	16	AR024289 Sequence
21	16	44.4	16	16	AR045142 Sequence
20	16	44.4	16	16	BD011366 Chimeric
19	16	44.4	16	16	E43836 Chimeric an
18	16	44.4	16	16	AR009777 Sequence
17	16	44.4	16	16	I89916 Sequence 33
16	16	44.4	16	16	AX224358 Sequence
15	16	44.4	16	16	AX326740 Sequence
14	16	44.4	16	16	AF166795 Hepatitis
13	16	44.4	16	16	AF166786 Hepatitis
12	16	44.4	16	16	AF166787 Hepatitis
11	16	44.4	16	16	AF166790 Hepatitis
10	16	44.4	16	16	AF166793 Hepatitis
9	16	44.4	16	16	AF166794 Hepatitis
8	16	44.4	16	16	AF166796 Hepatitis
7	16	44.4	16	16	AF166798 Hepatitis
6	16	44.4	16	16	AF166802 Hepatitis
5	16	44.4	16	16	AF166803 Hepatitis
4	16	44.4	16	16	AF166805 Hepatitis
3	16	44.4	16	16	U33798 Human Immat
2	16	44.4	16	16	286018 M.musculus
1	16	44.4	16	16	286020 M.musculus

74	15.8	43.9	33	6	AX015110	AX015110 Sequence	147	15	41.7	31	6	BD008334	BD008334 Inhibitin
75	15.6	43.3	38	6	I34370	I34370 Sequence 69	148	15	41.7	31	6	E23304	E23304 Antibody ag
76	15.6	43.3	40	6	AX167967	AX167967 Sequence	149	15	41.7	31	6	E27073	E27073 Remedy for
77	15.6	43.3	40	6	BD000227	BD000227 Cell for	150	15	41.7	36	6	A18355	A18355 Oligonucleo
78	15.6	43.3	40	6	BD006861	BD006861 Method fo	151	15	41.7	36	6	AR024287	AR024287 Sequence
79	15.6	43.3	42	6	HSU27250	HSU27250 Human isola	152	15	41.7	36	6	AR045140	AR045140 Sequence
80	15.4	42.8	59	6	I65783	I65783 Sequence 22	153	15	41.7	36	6	BD011364	BD011364 Chimeric
81	15.4	42.8	33	6	A62591	A62591 Sequence 10	154	15	41.7	36	6	E43834	E43834 Chimeric an
82	15.4	42.8	37	6	AX275051	AX275051 Sequence	155	15	41.7	37	6	AR091832	AR091832 Sequence
83	15.4	42.8	51	6	AX199213	AX199213 Sequence	156	15	41.7	37	6	AR157740	AR157740 Sequence
84	15.4	42.8	51	6	AX199215	AX199215 Sequence	157	15	41.7	38	6	AX068401	AX068401 Sequence
85	15.4	42.8	51	6	AX199493	AX199493 Sequence	158	15	41.7	41	6	AR162657	AR162657 Sequence
86	15.4	42.8	51	6	AX199495	AX199495 Sequence	159	15	41.7	41	6	BD005928	BD005928 Human B-c
87	15.4	42.8	51	6	AX199497	AX199497 Sequence	160	15	41.7	42	6	I15503	I15503 Sequence 4
88	15.4	42.8	66	6	AX199497	AX199497 Sequence	161	15	41.7	44	6	A38860	A38860 Sequence 14
89	15.4	42.8	70	6	CHRC1A212	CHRC1A212 Sequence	162	15	41.7	44	6	A47745	A47745 Sequence 3
90	15.4	42.8	70	6	E32644	E32644 Method for	163	15	41.7	44	6	A73049	A73049 Sequence 25
91	15.4	42.8	81	14	AF207402	AF207402 Hepatitis	164	15	41.7	44	6	A73141	A73141 Sequence 25
92	15.4	42.8	81	14	AF207403	AF207403 Hepatitis	165	15	41.7	44	6	AR013765	AR013765 Sequence
93	15.4	42.8	81	14	AF207405	AF207405 Hepatitis	166	15	41.7	44	6	AR093117	AR093117 Sequence
94	15.4	42.8	81	14	AF207407	AF207407 Hepatitis	167	15	41.7	44	6	AR126945	AR126945 Sequence
95	15.4	42.8	81	14	AF207408	AF207408 Hepatitis	168	15	41.7	44	6	AR174690	AR174690 Sequence
96	15.4	42.8	81	14	AF207409	AF207409 Hepatitis	169	15	41.7	50	6	AX199498	AX199498 Sequence
97	15.4	42.8	81	14	AF207411	AF207411 Hepatitis	170	15	41.7	51	6	AX157641	AX157641 Sequence
98	15.4	42.8	81	14	AF207412	AF207412 Hepatitis	171	15	41.7	51	6	AX158719	AX158719 Sequence
99	15.4	42.8	81	14	AF207413	AF207413 Hepatitis	172	15	41.7	51	6	AX158720	AX158720 Sequence
100	15.4	42.8	81	14	AF207415	AF207415 Hepatitis	173	15	41.7	51	6	AX158721	AX158721 Sequence
101	15.4	42.8	81	14	AF207416	AF207416 Hepatitis	174	15	41.7	51	6	AX158722	AX158722 Sequence
102	15.4	42.8	81	14	AF207417	AF207417 Hepatitis	175	15	41.7	55	6	A08730	A08730 Nucleotide
103	15.4	42.8	81	14	AF207418	AF207418 Hepatitis	176	15	41.7	55	6	A08731	A08731 reverse com
104	15.4	42.8	81	14	AF207420	AF207420 Hepatitis	177	15	41.7	55	6	A14751	A14751 Nucleotide
105	15.4	42.8	81	14	AF207421	AF207421 Hepatitis	178	15	41.7	55	6	A14752	A14752 Nucleotide
106	15.4	42.8	81	14	AF207422	AF207422 Hepatitis	179	15	41.7	58	6	A17932	A17932 Oligonucleo
107	15.4	42.8	81	14	AF207423	AF207423 Hepatitis	180	15	41.7	58	6	I24542	I24542 Sequence 22
108	15.4	42.8	81	14	AF207424	AF207424 Hepatitis	181	15	41.7	58	6	I33884	I33884 Sequence 23
109	15.4	42.8	81	14	AF207425	AF207425 Hepatitis	182	15	41.7	58	6	I56779	I56779 Sequence 2
110	15.4	42.8	81	14	AF207426	AF207426 Hepatitis	183	15	41.7	58	6	I83675	I83675 Sequence 4
111	15.4	42.8	81	14	AF207428	AF207428 Hepatitis	184	15	41.7	60	10	MM5HT3B1	MM5HT3B1 Mus muscu
112	15.4	42.8	81	14	AF207429	AF207429 Hepatitis	185	15	41.7	98	9	AB032815	AB032815 Homo sapi
113	15.4	42.8	81	14	AF207430	AF207430 Hepatitis	186	14.8	41.1	18	6	A06695	A06695 Oligonucleo
114	15.4	42.8	81	14	AF207431	AF207431 Hepatitis	187	14.8	41.1	18	6	A09999	A09999 Oligonucleo
115	15.4	42.8	81	14	AF207432	AF207432 Hepatitis	188	14.8	41.1	26	6	AR003614	AR003614 Sequence
116	15.4	42.8	81	14	AF207433	AF207433 Hepatitis	189	14.8	41.1	26	6	AR071163	AR071163 Sequence
117	15.4	42.8	81	14	AF207434	AF207434 Hepatitis	190	14.8	41.1	26	6	AR108164	AR108164 Sequence
118	15.4	42.8	81	14	AF207435	AF207435 Hepatitis	191	14.8	41.1	26	6	I22381	I22381 Sequence 7
119	15.4	42.8	81	14	AF207436	AF207436 Hepatitis	192	14.8	41.1	37	6	AX228583	AX228583 Sequence
120	15.4	42.8	81	14	AF207437	AF207437 Hepatitis	193	14.8	41.1	43	6	AR161407	AR161407 Sequence
121	15.4	42.8	81	14	AF207438	AF207438 Hepatitis	194	14.8	41.1	51	6	A00936	A00936 Nucleotide
122	15.4	42.8	81	14	AF207439	AF207439 Hepatitis	195	14.8	41.1	51	6	A00937	A00937 Nucleotide
123	15.4	42.8	81	14	AF207440	AF207440 Hepatitis	196	14.8	41.1	62	6	AR171487	AR171487 Sequence
124	15.4	42.8	81	14	AF207441	AF207441 Hepatitis	197	14.8	41.1	62	6	BD005507	BD005507 Compositi
125	15.4	42.8	89	5	CHRCOLA12	M25967 Chicken alp	198	14.8	41.1	77	10	M05JHCD3	M05JHCD3
126	15.4	42.8	93	6	AX327599	AX327599 Sequence	199	14.8	41.1	98	6	AX287660	AX287660 Sequence
127	15.2	42.2	28	6	AR055231	AR055231 Sequence	200	14.6	40.6	21	6	AX021251	AX021251 Sequence
128	15.2	42.2	35	6	I05643	I05643 Sequence 2	201	14.6	40.6	26	6	AR090181	AR090181 Sequence
129	15.2	42.2	37	6	AX219956	AX219956 Sequence	202	14.6	40.6	28	6	AR054129	AR054129 Sequence
130	15.2	42.2	37	6	AX228614	AX228614 Sequence	203	14.6	40.6	34	6	AX316603	AX316603 Sequence
131	15.2	42.2	47	6	AR070123	AR070123 Sequence	204	14.6	40.6	35	6	AX316601	AX316601 Sequence
132	15.2	42.2	51	6	AX118305	AX118305 Sequence	205	14.6	40.6	38	6	AB8352	AB8352 Sequence 78
133	15.2	42.2	51	6	AX158081	AX158081 Sequence	206	14.6	40.6	38	6	AX088706	AX088706 Sequence
134	15.2	42.2	51	6	AX158083	AX158083 Sequence	207	14.6	40.6	38	6	AX258833	AX258833 Sequence
135	15.2	42.2	51	6	AX159625	AX159625 Sequence	208	14.6	40.6	38	6	AX258836	AX258836 Sequence
136	15.2	42.2	51	6	AX161938	AX161938 Sequence	209	14.6	40.6	39	6	AR123938	AR123938 Sequence
137	15	41.7	17	6	BD004410	BD004410 Ameliorat	210	14.6	40.6	44	6	AX305183	AX305183 Sequence
138	15	41.7	17	6	BD004466	BD004466 Therapeut	211	14.6	40.6	48	6	AX244175	AX244175 Sequence
139	15	41.7	17	6	BD004527	BD004527 Therapeut	212	14.6	40.6	50	6	AX161637	AX161637 Sequence
140	15	41.7	17	6	BD008360	BD008360 Inhibitin	213	14.6	40.6	51	6	AX117469	AX117469 Sequence
141	15	41.7	17	6	E23330	E23330 Antibody ag	214	14.6	40.6	51	6	AX161995	AX161995 Sequence
142	15	41.7	17	6	E27099	E27099 Remedy for	215	14.6	40.6	51	6	AX161996	AX161996 Sequence
143	15	41.7	26	6	AX151539	AX151539 Sequence	216	14.6	40.6	80	11	H0MUP950B	H0MUP950B
144	15	41.7	31	6	BD004384	BD004384 Ameliorat	217	14.6	40.6	81	14	AB001403	AB001403 Hepatitis
145	15	41.7	31	6	BD004440	BD004440 Therapeut	218	14.6	40.6	81	14	AF166574	AF166574 Hepatitis
146	15	41.7	31	6	BD004501	BD004501 Therapeut	219	14.6	40.6	81	14	AF166586	AF166586 Hepatitis



220	14.6	40.6	86	6	AR042750	AR042750 Sequence	C	293	14.2	39.4	56	9	HUMNTCOR02	U84641 Human putat	
221	14.6	40.6	100	9	ARJ8162	AI008162 Homo sapi		294	14.2	39.4	57	6	A02051	AI02051 Artificial	
222	14.4	40.0	20	6	AR091863	AR091863 Sequence		295	14.2	39.4	70	14	REO3M2A	AI024291 Reovirus se	
223	14.4	40.0	25	6	AR157771	AR157771 Sequence		296	14.2	39.4	87	6	A42449	AI2449 Sequence 31	
c	224	14.4	40.0	25	6	IE5383	IE5383 Sequence 6	c	297	14.2	39.4	90	10	RNU76221	U76221 Rattus norv
225	14.4	40.0	30	6	BD004404	BD004404 Ameliorat		298	14.2	39.4	96	6	E05300	E05300 DNA encodin	
226	14.4	40.0	30	6	BD004460	BD004460 Therapeut		299	14.2	39.4	99	6	AX050409	AX050409 Sequence	
227	14.4	40.0	30	6	BD004521	BD004521 Therapeut		300	14.2	39.4	100	6	AX287667	AX287667 Sequence	
228	14.4	40.0	30	6	BD008354	BD008354 Inhibitin		301	14	38.9	33	6	A52067	A52067 Sequence 23	
229	14.4	40.0	30	6	E23324	E23324 Antibody ag		302	14	38.9	33	6	AR004371	AR004371 Sequence	
230	14.4	40.0	30	6	E27093	E27093 Remedy for		303	14	38.9	33	6	AR067676	AR067676 Sequence	
231	14.4	40.0	32	6	AR024308	AR024308 Sequence		304	14	38.9	33	6	AR097162	AR097162 Sequence	
232	14.4	40.0	32	6	AR045161	AR045161 Sequence		305	14	38.9	33	6	AR130660	AR130660 Sequence	
233	14.4	40.0	32	6	AR165166	AR165166 Sequence		306	14	38.9	33	6	AR169821	AR169821 Sequence	
234	14.4	40.0	32	6	AX114312	AX114312 Sequence		307	14	38.9	33	6	AR172009	AR172009 Sequence	
235	14.4	40.0	32	6	BD011385	BD011385 Chimeric		308	14	38.9	33	6	I82846	I82846 Sequence 25	
236	14.4	40.0	32	6	E43855	E43855 Chimeric an		309	14	38.9	34	6	AK102293	AK102293 Sequence	
237	14.4	40.0	33	6	I15509	I15509 Sequence 4		310	14	38.9	35	6	BD004398	BD004398 Ameliorat	
238	14.4	40.0	33	6	I89331	I89331 Sequence 4		311	14	38.9	35	6	BD004454	BD004454 Therapeut	
239	14.4	40.0	36	6	AR024282	AR024282 Sequence		312	14	38.9	35	6	BD004515	BD004515 Therapeut	
240	14.4	40.0	36	6	AR045135	AR045135 Sequence		313	14	38.9	35	6	BD008348	BD008348 Inhibitin	
241	14.4	40.0	36	6	BD004386	BD004386 Ameliorat		314	14	38.9	35	6	E23318	E23318 Antibody ag	
242	14.4	40.0	36	6	BD004442	BD004442 Therapeut		315	14	38.9	35	6	E27087	E27087 Remedy for	
243	14.4	40.0	36	6	BD004503	BD004503 Therapeut	C	316	14	38.9	37	6	A18356	A18356 Oligonucleo	
244	14.4	40.0	36	6	BD008336	BD008336 Inhibitin		317	14	38.9	37	6	AR091839	AR091839 Sequence	
245	14.4	40.0	36	6	BD011359	BD011359 Chimeric		318	14	38.9	37	6	AR157747	AR157747 Sequence	
246	14.4	40.0	36	6	E23306	E23306 Antibody ag		319	14	38.9	37	6	AX228606	AX228606 Sequence	
247	14.4	40.0	36	6	E27075	E27075 Remedy for		320	14	38.9	38	6	AR016264	AR016264 Sequence	
248	14.4	40.0	36	6	E43829	E43829 Chimeric an		321	14	38.9	38	6	AX006415	AX006415 Sequence	
249	14.4	40.0	45	6	AX323471	AX323471 Sequence	C	322	14	38.9	40	6	AR042818	AR042818 Sequence	
c	250	14.4	40.0	45	6	I34331	I34331 Sequence 30		323	14	38.9	40	6	AX224357	AX224357 Sequence
c	251	14.4	51	6	AX159454	AX159454 Sequence	C	324	14	38.9	40	6	AX224362	AX224362 Sequence	
c	252	14.4	40.0	51	6	ARX52746	ARX52746 Sequence	C	325	14	38.9	41	6	A80778	A80778 Sequence 33
253	14.4	40.0	55	6	AR067956	AR067956 Sequence	C	326	14	38.9	41	6	AX022742	AX022742 Sequence	
254	14.4	40.0	55	6	AR078911	AR078911 Sequence		327	14	38.9	41	6	AX077736	AX077736 Sequence	
255	14.4	40.0	55	6	AR097705	AR097705 Sequence		328	14	38.9	41	6	AX224360	AX224360 Sequence	
c	256	14.4	59	6	AX326761	AX326761 Sequence		329	14	38.9	42	6	AR016270	AR016270 Sequence	
c	257	14.4	40.0	60	6	AR125904	AR125904 Sequence		330	14	38.9	42	6	AX077754	AX077754 Sequence
c	258	14.4	40.0	60	6	I24271	I24271 Sequence 58		331	14	38.9	42	6	AX077755	AX077755 Sequence
c	259	14.4	40.0	66	9	AF189388	AF189388 Homo sapi		332	14	38.9	43	6	AX301771	AX301771 Sequence
260	14.4	40.0	68	6	AX002785	AX002785 Sequence		333	14	38.9	47	6	AX194988	AX194988 Sequence	
261	14.4	40.0	68	6	AX148541	AX148541 Sequence	C	334	14	38.9	50	6	AX194994	AX194994 Sequence	
262	14.4	40.0	72	6	A94096	A94096 Sequence 77	C	335	14	38.9	50	6	AX199496	AX199496 Sequence	
c	263	14.4	40.0	72	6	AX011181	AX011181 Sequence	C	336	14	38.9	51	6	AX157962	AX157962 Sequence
c	264	14.4	40.0	74	6	I34325	I34325 Sequence 24	C	337	14	38.9	51	6	AX190219	AX190219 Sequence
c	265	14.4	81	14	AF166799	AF166799 Hepatitis		338	14	38.9	54	6	A17931	A17931 Oligonucleo	
c	266	14.4	40.0	81	14	AF166800	AF166800 Hepatitis		339	14	38.9	54	6	A38679	A38679 Sequence 10
c	267	14.4	40.0	93	9	HUMRH01	LI4658 Human funar		340	14	38.9	54	6	I24541	I24541 Sequence 21
c	268	14.4	40.0	94	5	AF272967	AF272967 Mastacemb		341	14	38.9	54	6	I33883	I33883 Sequence 22
c	269	14.4	40.0	94	5	AF272968	AF272968 Mastacemb		342	14	38.9	54	6	I56778	I56778 Sequence 1
c	270	14.4	40.0	98	6	AR162990	AR162990 Sequence		343	14	38.9	54	6	I83674	I83674 Sequence 3
c	271	14.4	40.0	98	6	AR162991	AR162991 Sequence		344	14	38.9	55	6	AR003615	AR003615 Sequence
272	14.2	39.4	23	6	A61986	A61986 Sequence 16		345	14	38.9	55	6	AR071164	AR071164 Sequence	
273	14.2	39.4	25	6	AX117172	AX117172 Sequence		346	14	38.9	56	6	AR108165	AR108165 Sequence	
274	14.2	39.4	27	6	I04405	I04405 Sequence 3		347	14	38.9	56	6	I22382	I22382 Sequence 8	
275	14.2	39.4	27	6	I04434	I04434 Sequence 32	C	348	14	38.9	57	6	AX180944	AX180944 Sequence	
c	276	14.2	29	6	AX183868	AX183868 Sequence	C	349	14	38.9	57	6	I01657	I01657 Sequence 2	
c	277	14.2	31	6	AX247956	AX247956 Sequence	C	350	14	38.9	66	9	HSU91015	HSU91015 Homo saplen	
c	278	14.2	32	6	A73580	A73580 Sequence 4	C	351	14	38.9	75	8	YSCGTGMA	YSCGTGMA Yeast tRNA-	
279	14.2	39.4	33	6	AR104469	AR104469 Sequence	C	352	14	38.9	81	4	AR042783	AR042783 Sequence	
280	14.2	39.4	33	6	AR104470	AR104470 Sequence	C	353	14	38.9	88	4	BR08646	BR08646 Bos taurus	
281	14.2	39.4	36	6	AX004141	AX004141 Sequence	C	354	14	38.9	90	9	S80930	S80930 Rattus norv	
282	14.2	39.4	40	6	AR162661	AR162661 Sequence	C	355	14	38.9	90	10	RNDRSLV13	U030811 Rattus norv	
283	14.2	39.4	40	6	BD005932	BD005932 Human B-c	C	356	14	38.9	98	6	I91504	I91504 Sequence 38	
284	14.2	39.4	46	6	A98781	A98781 Sequence 14	C	357	14	38.9	100	12	SYNNSAA02	M36611 Synthetic h	
285	14.2	39.4	51	6	AX117173	AX117173 Sequence	C	358	13.8	38.3	30	6	AX224739	AX224739 Sequence	
286	14.2	39.4	51	6	AX118349	AX118349 Sequence	C	359	13.8	38.3	31	6	A06220	A06220 Synthetic D	
c	287	14.2	51	6	AX158947	AX158947 Sequence	C	360	13.8	38.3	31	6	AX249029	AX249029 Sequence	
288	14.2	39.4	51	6	AX161817	AX161817 Sequence		361	13.8	38.3	32	6	AX101289	AX101289 Sequence	
289	14.2	39.4	51	6	AX161819	AX161819 Sequence		362	13.8	38.3	36	6	AR055641	AR055641 Sequence	
290	14.2	39.4	51	6	AX161821	AX161821 Sequence		363	13.8	38.3	36	6	AR071955	AR071955 Sequence	
291	14.2	39.4	51	6	AX161823	AX161823 Sequence		364	13.8	38.3	36	6	I05897	I05897 Sequence 13	
292	14.2	39.4	51	6	AX161824	AX161824 Sequence		365	13.8	38.3	36	6	I31786	I31786 Sequence 6	

C 366	13.8	38.3	37	6	AX228560	AX228560 Sequence	C 439	13.6	37.8	34	6	AX106941	AX106941 Sequence
C 367	13.8	38.3	43	6	AX62205	A62205 Sequence 99	C 440	13.6	37.8	34	6	AX137871	AX137871 Sequence
C 368	13.8	38.3	43	6	AX006967	AX006967 Sequence	C 441	13.6	37.8	36	6	A27939	A27939 Primer to 1
C 369	13.8	38.3	43	6	AX022429	AX022429 Sequence	C 442	13.6	37.8	36	6	AR129809	AR129809 Sequence
C 370	13.8	38.3	45	6	I49788	I49788 Sequence 11	C 443	13.6	37.8	36	6	AX043838	AX043838 Sequence
C 371	13.8	38.3	46	6	AX044483	AX044483 Sequence	C 444	13.6	37.8	36	6	AX081224	AX081224 Sequence
C 372	13.8	38.3	50	6	AR032776	AR032776 Sequence	C 445	13.6	37.8	36	6	AX090374	AX090374 Sequence
C 373	13.8	38.3	50	6	I29516	I29516 Sequence 38	C 446	13.6	37.8	36	6	E36458	E36458 DNA polymer
C 374	13.8	38.3	50	6	I91190	I91190 Sequence 38	C 447	13.6	37.8	36	6	I13359	I13359 Sequence 16
C 375	13.8	38.3	51	6	AX117685	AX117685 Sequence	C 448	13.6	37.8	36	6	I26292	I26292 Sequence 41
C 376	13.8	38.3	51	6	AX117713	AX117713 Sequence	C 449	13.6	37.8	37	6	AX077740	AX077740 Sequence
C 377	13.8	38.3	51	6	AX190062	AX190062 Sequence	C 450	13.6	37.8	37	6	AX220003	AX220003 Sequence
C 378	13.8	38.3	51	6	AX190064	AX190064 Sequence	C 451	13.6	37.8	37	6	AX223014	AX223014 Sequence
C 379	13.8	38.3	51	6	AX199214	AX199214 Sequence	C 452	13.6	37.8	37	6	AX228541	AX228541 Sequence
C 380	13.8	38.3	51	6	AX199216	AX199216 Sequence	C 453	13.6	37.8	38	6	AX077753	AX077753 Sequence
C 381	13.8	38.3	54	6	AX080406	AX080406 Sequence	C 454	13.6	37.8	39	6	AX077739	AX077739 Sequence
C 382	13.8	38.3	57	6	AX040789	AX040789 Sequence	C 455	13.6	37.8	39	6	AX118782	AX118782 Sequence
C 383	13.8	38.3	60	6	AR028966	AR028966 Sequence	C 456	13.6	37.8	39	6	AX224259	AX224259 Sequence
C 384	13.8	38.3	60	6	AR028967	AR028967 Sequence	C 457	13.6	37.8	40	6	AB4405	AB4405 Sequence 20
C 385	13.8	38.3	60	6	AR156848	AR156848 Sequence	C 458	13.6	37.8	41	6	BD004387	BD004387 Ameliorat
C 386	13.8	38.3	60	6	AR156849	AR156849 Sequence	C 459	13.6	37.8	41	6	BD004443	BD004443 Therapeut
C 387	13.8	38.3	62	14	HS5TRLE	HS5277 Human cytom	C 460	13.6	37.8	41	6	BD004504	BD004504 Therapeut
C 388	13.8	38.3	73	1	BA1R0601	M79433 Bacterium T	C 461	13.6	37.8	41	6	BD008337	BD008337 Inhibitin
C 389	13.8	38.3	74	1	FSPI651	X53208 Frankia spe	C 462	13.6	37.8	41	6	E23307	E23307 Antibody ag
C 390	13.8	38.3	74	1	KA1651	X53190 Kibdelospor	C 463	13.6	37.8	41	6	E27076	E27076 Remedy for
C 391	13.8	38.3	74	1	SA1651	X53192 Saccharothr	C 464	13.6	37.8	45	6	AR085458	AR085458 Sequence
C 392	13.8	38.3	75	6	AX252335	AX252335 Sequence	C 465	13.6	37.8	45	6	AR088864	AR088864 Sequence
C 393	13.8	38.3	76	10	AF265802	AF265802 Mus muscu	C 466	13.6	37.8	45	6	AR167338	AR167338 Sequence
C 394	13.8	38.3	79	9	HUMGBPA1	K00092 Human chor	C 467	13.6	37.8	45	6	AX100526	AX100526 Sequence
C 395	13.8	38.3	80	6	I34322	I34322 Sequence 21	C 468	13.6	37.8	45	6	E60002	E60002 Ceramide-b1
C 396	13.8	38.3	81	14	AF166630	AF166630 Hepatitis	C 469	13.6	37.8	45	6	I36721	I36721 Sequence 30
C 397	13.8	38.3	81	14	AF207406	AF207406 Hepatitis	C 470	13.6	37.8	48	6	A99028	A99028 Sequence 36
C 398	13.8	38.3	81	14	AF202427	AF202427 Hepatitis	C 471	13.6	37.8	50	6	AX165046	AX165046 Sequence
C 399	13.8	38.3	86	6	AR152216	AR152216 Sequence	C 472	13.6	37.8	51	6	AX115625	AX115625 Sequence
C 400	13.8	38.3	86	6	AX039231	AX039231 Sequence	C 473	13.6	37.8	51	6	AX158082	AX158082 Sequence
C 401	13.8	38.3	86	6	AX039471	AX039471 Sequence	C 474	13.6	37.8	51	6	AX158084	AX158084 Sequence
C 402	13.8	38.3	86	6	AX134829	AX134829 Sequence	C 475	13.6	37.8	51	6	AX158561	AX158561 Sequence
C 403	13.8	38.3	86	6	AX134918	AX134918 Sequence	C 476	13.6	37.8	51	6	AX159626	AX159626 Sequence
C 404	13.8	38.3	86	6	AX135037	AX135037 Sequence	C 477	13.6	37.8	51	6	AX160752	AX160752 Sequence
C 405	13.8	38.3	87	6	AX039233	AX039233 Sequence	C 478	13.6	37.8	51	6	AX161937	AX161937 Sequence
C 406	13.8	38.3	87	6	AX039473	AX039473 Sequence	C 479	13.6	37.8	51	6	AX164880	AX164880 Sequence
C 407	13.8	38.3	87	6	AX134831	AX134831 Sequence	C 480	13.6	37.8	51	6	AX165565	AX165565 Sequence
C 408	13.8	38.3	87	6	AX134920	AX134920 Sequence	C 481	13.6	37.8	51	6	AX204340	AX204340 Sequence
C 409	13.8	38.3	87	6	AX135039	AX135039 Sequence	C 482	13.6	37.8	55	9	HUMDF12M3	HUMDF12M3 Sequence
C 410	13.8	38.3	96	6	AR152241	AR152241 Sequence	C 483	13.6	37.8	56	6	A36725	A36725 Sequence 4
C 411	13.6	37.8	20	6	AX182206	AX182206 Sequence	C 484	13.6	37.8	60	6	I04854	I04854 Sequence 13
C 412	13.6	37.8	21	6	AX097256	AX097256 Sequence	C 485	13.6	37.8	70	9	H006874S03	H006874S03 Sequence
C 413	13.6	37.8	21	6	AX224361	AX224361 Sequence	C 486	13.6	37.8	74	6	AX277135	AX277135 Sequence
C 414	13.6	37.8	22	6	E32640	E32640 Method for	C 487	13.6	37.8	80	6	AR042778	AR042778 Sequence
C 415	13.6	37.8	24	6	AX119402	AX119402 Sequence	C 488	13.6	37.8	80	14	MCPRNA3A	MCPRNA3A Sequence
C 416	13.6	37.8	25	6	AR085680	AR085680 Sequence	C 489	13.6	37.8	81	14	AF168866	AF168866 Sequence
C 417	13.6	37.8	25	6	AX279037	AX279037 Sequence	C 490	13.6	37.8	84	6	AX010625	AX010625 Sequence
C 418	13.6	37.8	28	6	E39126	E39126 Porous flbe	C 491	13.6	37.8	85	6	AX023590	AX023590 Sequence
C 419	13.6	37.8	28	6	E39437	E39437 Hollow flbe	C 492	13.6	37.8	90	6	AX210133	AX210133 Sequence
C 420	13.6	37.8	28	6	E39441	E39441 Fiber carry	C 493	13.6	37.8	90	9	HUMTCRABE	HUMTCRABE Sequence
C 421	13.6	37.8	28	6	E41581	E41581 Nucleic aci	C 494	13.6	37.8	100	10	HAMBRN2	HAMBRN2 Sequence
C 422	13.6	37.8	28	6	E50121	E50121 Porous holl	C 495	13.6	37.8	100	10	RNO230479	RNO230479 Sequence
C 423	13.6	37.8	28	6	E59661	E59661 Laminate of	C 496	13.4	37.2	24	6	AR018080	AR018080 Sequence
C 424	13.6	37.8	28	6	E59665	E59665 Laminate of	C 497	13.4	37.2	24	6	AR051920	AR051920 Sequence
C 425	13.6	37.8	28	6	E64338	E64338 Nucleic aci	C 498	13.4	37.2	25	6	AX147164	AX147164 Sequence
C 426	13.6	37.8	32	6	A44587	A44587 Sequence 3	C 499	13.4	37.2	25	6	E12633	E12633 DNA oligome
C 427	13.6	37.8	32	6	A50872	A50872 Sequence 5	C 500	13.4	37.2	27	6	A65605	A65605 Sequence 3
C 428	13.6	37.8	32	6	AR075549	AR075549 Sequence	C 501	13.4	37.2	27	6	AR109670	AR109670 Sequence
C 429	13.6	37.8	33	6	E39124	E39124 Porous flbe	C 502	13.4	37.2	28	6	AX008134	AX008134 Sequence
C 430	13.6	37.8	33	6	E39435	E39435 Hollow flbe	C 503	13.4	37.2	28	6	AX008136	AX008136 Sequence 12
C 431	13.6	37.8	33	6	E39439	E39439 Fiber carry	C 504	13.4	37.2	29	6	AX039170	AX039170 Sequence
C 432	13.6	37.8	33	6	E41579	E41579 Nucleic aci	C 505	13.4	37.2	30	6	BD001122	BD001122 Method an
C 433	13.6	37.8	33	6	E50119	E50119 Porous holl	C 506	13.4	37.2	30	6	BD001151	BD001151 Method an
C 434	13.6	37.8	33	6	E59659	E59659 Laminate of	C 507	13.4	37.2	31	6	AR098846	AR098846 Sequence
C 435	13.6	37.8	33	6	E59663	E59663 Laminate of	C 508	13.4	37.2	34	6	A40137	A40137 Sequence 13
C 436	13.6	37.8	33	6	E64336	E64336 Nucleic aci	C 509	13.4	37.2	34	23	E10960	E10960 Primer . 9/2
C 437	13.6	37.8	34	6	A40137	A40137 Sequence 13	C 510	13.4	37.2	35	11	C75828	C75828 Homo saplen
C 438	13.6	37.8	34	6	A93588	A93588 Sequence 18	C 511	13.4	37.2	37	6	AR091581	AR091581 Sequence

512	13.4	37.2	37	6	AR091583	AR091583 Sequence	C 585	13.2	36.7	37	6	172077	172077 Sequence 1
513	13.4	37.2	41	6	AR096931	AR096931 Sequence	586	13.2	36.7	38	6	AR169927	AR169927 Sequence
514	13.4	37.2	45	6	AX201011	AX201011 Sequence	587	13.2	36.7	38	6	AX235259	AX235259 Sequence
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517	13.4	37.2	45	6	AX267811	AX267811 Sequence	590	13.2	36.7	41	6	AR108513	AR108513 Sequence
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519	13.4	37.2	51	6	AX117269	AX117269 Sequence	592	13.2	36.7	41	6	116470	116470 Sequence 29
520	13.4	37.2	51	6	AX158201	AX158201 Sequence	593	13.2	36.7	41	6	169556	169556 Sequence 29
521	13.4	37.2	51	6	AX159227	AX159227 Sequence	594	13.2	36.7	41	6	185050	185050 Sequence 29
522	13.4	37.2	51	9	HSA132926	AX132926 Homo sapi	595	13.2	36.7	44	6	AR008958	AR008958 Sequence
523	13.4	37.2	58	6	AR048625	AR048625 Sequence	596	13.2	36.7	44	6	AR013766	AR013766 Sequence
524	13.4	37.2	60	6	AR121644	AR121644 Sequence	597	13.2	36.7	44	6	124412	124412 Sequence 7
525	13.4	37.2	60	6	ES5391	ES5391 Process for	598	13.2	36.7	45	6	AR92629	AR92629 Sequence 1
526	13.4	37.2	66	6	AX179470	AX179470 Sequence	599	13.2	36.7	45	6	AR071264	AR071264 Sequence
527	13.4	37.2	69	6	AR052653	AR052653 Sequence	600	13.2	36.7	45	6	AR152959	AR152959 Sequence
528	13.4	37.2	71	6	A60841	A60841 Sequence 15	601	13.2	36.7	45	6	AR166071	AR166071 Sequence
529	13.4	37.2	74	9	S74825	S74825 RET...ELF1	602	13.2	36.7	45	6	AX164014	AX164014 Sequence
530	13.4	37.2	75	1	ECTRNE5U	X05359 E.coli tRNA	603	13.2	36.7	46	6	AX076698	AX076698 Sequence
531	13.4	37.2	76	8	SOBTREPA	M5610 S.obliquus	604	13.2	36.7	46	6	AX076699	AX076699 Sequence
532	13.4	37.2	81	6	A23330	A23320 oligonucleo	605	13.2	36.7	46	6	AX076700	AX076700 Sequence
533	13.4	37.2	81	6	AR013746	AR013746 Sequence	606	13.2	36.7	46	6	AX076701	AX076701 Sequence
534	13.4	37.2	81	6	AR174706	AR174706 Sequence	607	13.2	36.7	46	6	AX076702	AX076702 Sequence
535	13.4	37.2	83	4	RABPRKM1B	M14473 RabbIt Musc	608	13.2	36.7	46	6	AX076703	AX076703 Sequence
536	13.4	37.2	86	6	AX038232	AX039232 Sequence	609	13.2	36.7	48	6	A23087	A23087 Sequence
537	13.4	37.2	86	6	AX039472	AX039472 Sequence	610	13.2	36.7	48	6	A23087	A23087 Sequence
538	13.4	37.2	86	6	AX134830	AX134830 Sequence	611	13.2	36.7	48	6	A23087	A23087 Sequence
539	13.4	37.2	86	6	AX134919	AX134919 Sequence	612	13.2	36.7	48	6	A24285	A24285 Sequence
540	13.4	37.2	86	6	AX135038	AX135038 Sequence	613	13.2	36.7	48	6	AR028593	AR028593 Sequence
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542	13.4	37.2	87	6	AX039474	AX039474 Sequence	615	13.2	36.7	48	6	AR084955	AR084955 Sequence
543	13.4	37.2	87	6	AX134832	AX134832 Sequence	616	13.2	36.7	48	6	AR085804	AR085804 Sequence
544	13.4	37.2	87	6	AX134921	AX134921 Sequence	617	13.2	36.7	48	6	AX010634	AX010634 Sequence
545	13.4	37.2	87	6	AX135040	AX135040 Sequence	618	13.2	36.7	48	6	E31323	E31323 Process for
546	13.4	37.2	89	6	AR162979	AR162979 Sequence	619	13.2	36.7	48	6	119135	119135 Sequence 33
547	13.4	37.2	92	6	AX209072	AX209072 Sequence	620	13.2	36.7	49	6	143038	143038 Sequence 21
548	13.4	37.2	94	6	AX326633	AX326633 Sequence	621	13.2	36.7	49	9	HSU30447	HSU30447 Human Isola
549	13.4	37.2	94	6	AX326634	AX326634 Sequence	622	13.2	36.7	50	6	AX097523	AX097523 Sequence
550	13.4	37.2	94	6	AX326658	AX326658 Sequence	623	13.2	36.7	50	6	AX279653	AX279653 Sequence
551	13.4	37.2	94	6	AX326671	AX326671 Sequence	624	13.2	36.7	51	6	AX156906	AX156906 Sequence
552	13.4	37.2	100	9	AX8139	AX008139 Homo sapi	625	13.2	36.7	51	6	AX156498	AX156498 Sequence
553	13.2	36.7	18	6	EO6995	EO6995 5'primer to	626	13.2	36.7	51	6	AX161815	AX161815 Sequence
554	13.2	36.7	19	6	AX130953	AX130953 Sequence	627	13.2	36.7	51	6	AX162278	AX162278 Sequence
555	13.2	36.7	20	6	AX116329	AX116329 Sequence	628	13.2	36.7	51	6	AX162635	AX162635 Sequence
556	13.2	36.7	20	6	AR121479	AR121479 Sequence	629	13.2	36.7	51	6	AX163179	AX163179 Sequence
557	13.2	36.7	20	6	AR121480	AR121480 Sequence	630	13.2	36.7	51	6	AX163180	AX163180 Sequence
558	13.2	36.7	20	6	EO4077	EO4077 Primer for	631	13.2	36.7	51	6	AX165117	AX165117 Sequence
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560	13.2	36.7	24	6	E13472	E13472 PCR primer	633	13.2	36.7	51	6	AX199234	AX199234 Sequence
561	13.2	36.7	27	6	AR040342	AR040342 Sequence	634	13.2	36.7	51	6	105584	105584 Sequence 15
562	13.2	36.7	27	6	E12636	E12636 DNA oligome	635	13.2	36.7	52	6	AX150268	AX150268 Sequence
563	13.2	36.7	30	6	A02053	A02053 Artificial	636	13.2	36.7	55	6	106069	106069 Sequence 16
564	13.2	36.7	30	6	AR024327	AR024327 Sequence	637	13.2	36.7	56	6	106070	106070 Sequence 17
565	13.2	36.7	30	6	AR045180	AR045180 Sequence	638	13.2	36.7	56	12	SYNPLECA	SYNPLECA
566	13.2	36.7	30	6	AX100545	AX100545 Sequence	639	13.2	36.7	57	6	A02005	A02005 Artificial
567	13.2	36.7	30	6	BD011404	BD011404 Chimeric	640	13.2	36.7	57	6	A06451	A06451 Artificial
568	13.2	36.7	30	6	E43874	E43874 Chimeric an	641	13.2	36.7	58	6	AR055542	AR055542 Sequence
569	13.2	36.7	31	6	AR048182	AR048182 Sequence	642	13.2	36.7	58	6	AR082726	AR082726 Sequence
570	13.2	36.7	31	6	AX135237	AX135237 Sequence	643	13.2	36.7	58	6	AR084868	AR084868 Sequence
571	13.2	36.7	31	6	AX151286	AX151286 Sequence	644	13.2	36.7	58	6	AR087676	AR087676 Sequence
572	13.2	36.7	32	6	A08190	A08190 Oligonucleo	645	13.2	36.7	58	6	AR094036	AR094036 Sequence
573	13.2	36.7	32	6	E31942	E31942 Seven-pass	646	13.2	36.7	60	6	A29456	A29456 Sequence ex
574	13.2	36.7	33	6	AR100744	AR100744 Sequence	647	13.2	36.7	60	6	AR028968	AR028968 Sequence
575	13.2	36.7	33	6	AR125614	AR125614 Sequence	648	13.2	36.7	60	6	AR029899	AR029899 Sequence
576	13.2	36.7	33	6	AR130199	AR130199 Sequence	649	13.2	36.7	60	6	AR156850	AR156850 Sequence
577	13.2	36.7	36	6	AX094463	AX094463 Sequence	650	13.2	36.7	60	6	AX156851	AX156851 Sequence
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579	13.2	36.7	36	6	BD007707	BD007707 Dioxin re	652	13.2	36.7	62	6	AR171489	AR171489 Sequence
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581	13.2	36.7	37	6	AX219949	AX219949 Sequence	654	13.2	36.7	62	6	105585	105585 Sequence 16
582	13.2	36.7	37	6	AX220081	AX220081 Sequence	655	13.2	36.7	64	6	144603	144603 Sequence 32
583	13.2	36.7	37	6	AX220122	AX220122 Sequence	656	13.2	36.7	64	6	171008	171008 Sequence
584	13.2	36.7	37	6	AX228613	AX228613 Sequence	657	13.2	36.7	64	8	AF129578	AF129578 Racomilitri

C 658	13.2	36.7	66	0	104136	Sequence 24	731	13	36.1	32	6	AX137632	AX137632 Sequence
C 659	13.2	36.7	67	6	AR061632	Sequence	732	13	36.1	33	6	AX326580	AX326580 Sequence
C 660	13.2	36.7	67	6	AR108531	Sequence	733	13	36.1	34	6	AR056502	AR056502 Sequence
C 661	13.2	36.7	67	6	AX286215	Sequence	734	13	36.1	34	6	AR065614	AR065614 Sequence
C 662	13.2	36.7	67	6	116488	Sequence 31	735	13	36.1	36	6	AR018937	AR018937 Sequence
C 663	13.2	36.7	67	6	166974	Sequence 31	736	13	36.1	36	6	AR066565	AR066565 Sequence
C 664	13.2	36.7	67	6	185068	Sequence 31	737	13	36.1	36	6	172282	172282 Sequence 64
C 665	13.2	36.7	74	3	DME426972	Drosophila	738	13	36.1	36	6	176849	176849 Sequence 64
C 666	13.2	36.7	74	6	AX089704	Sequence	739	13	36.1	37	6	AX219933	AX219933 Sequence
C 667	13.2	36.7	74	6	AX090159	Sequence	740	13	36.1	37	6	AX220095	AX220095 Sequence
C 668	13.2	36.7	75	6	S59798S17	Sequence	741	13	36.1	38	6	AX350544	AX350544 Sequence
C 669	13.2	36.7	75	6	A20281	PKLR-L-type	742	13	36.1	38	6	E36560	E36560 Vector for
C 670	13.2	36.7	75	6	A20282	oligonucleo	743	13	36.1	39	6	AR026875	AR026875 Sequence
C 671	13.2	36.7	77	9	HSSRCE9	XO3997 Human c-src	744	13	36.1	39	6	AR049301	AR049301 Sequence
C 672	13.2	36.7	80	11	DM164C3T	Z71123 D. melanoga	745	13	36.1	39	6	AR065559	AR065559 Sequence
C 673	13.2	36.7	81	6	A20283	A20283 oligonucleo	746	13	36.1	39	6	AR118111	AR118111 Sequence
C 674	13.2	36.7	81	14	AF221161	Hepatitis	747	13	36.1	39	10	MM29299475	MM29299475 Mus muscu
C 675	13.2	36.7	81	14	AF221163	Hepatitis	748	13	36.1	41	6	AR127573	AR127573 Sequence
C 676	13.2	36.7	81	14	AF221164	Hepatitis	749	13	36.1	42	6	A27187	A27187 Oligonucleo
C 677	13.2	36.7	81	14	AF221165	Hepatitis	750	13	36.1	42	6	AR058955	AR058955 Sequence
C 678	13.2	36.7	81	14	AF221409	Hepatitis	751	13	36.1	42	6	AR105229	AR105229 Sequence
C 679	13.2	36.7	82	6	AR175473	Sequence	752	13	36.1	42	6	AR119150	AR119150 Sequence
C 680	13.2	36.7	82	6	AR175474	Sequence	753	13	36.1	42	6	AR123521	AR123521 Sequence
C 681	13.2	36.7	82	6	AR175475	Sequence	754	13	36.1	42	6	AR138174	AR138174 Sequence
C 682	13.2	36.7	84	6	AR041032	Sequence	755	13	36.1	42	6	AR176735	AR176735 Sequence
C 683	13.2	36.7	84	6	AF312274	Homo sapi	756	13	36.1	42	6	AX300421	AX300421 Sequence
C 684	13.2	36.7	85	4	OCT90	V00900 Rabbit trop	757	13	36.1	42	10	MMTCRBEF4	MMTCRBEF4 X70761 M. musculus
C 685	13.2	36.7	85	10	MMV156X1	269822 M.musculus	758	13	36.1	43	6	AR050860	AR050860 Sequence
C 686	13.2	36.7	85	10	RATRS1	K00370 Rat Ser-trp	759	13	36.1	43	6	E07917	E07917 Synthetic D
C 687	13.2	36.7	85	10	RNTNSER	X02685 Rat (BUF) t	760	13	36.1	46	6	E12821	E12821 PCR primer
C 688	13.2	36.7	86	6	AR140846	Sequence	761	13	36.1	46	6	I26191	I26191 Sequence 24
C 689	13.2	36.7	86	6	AR150796	Sequence	762	13	36.1	48	6	AR012090	AR012090 Sequence
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C 950 12.8 35.6 70 3 TF28SRNAB  
 C 951 12.8 35.6 73 6 ARI29049  
 C 952 12.8 35.6 73 6 ARI29049  
 C 953 12.8 35.6 73 6 E17115  
 C 954 12.8 35.6 73 6 E26013  
 C 955 12.8 35.6 73 6 E32123  
 C 956 12.8 35.6 75 6 E16727  
 C 957 12.8 35.6 75 6 E17116  
 C 958 12.8 35.6 75 6 E26014  
 C 959 12.8 35.6 75 6 E32124  
 C 960 12.8 35.6 76 11 H0MT7883A  
 C 961 12.8 35.6 78 3 AV013989  
 C 962 12.8 35.6 78 6 A37066  
 C 963 12.8 35.6 78 6 A37067  
 C 964 12.8 35.6 78 6 HUMM101  
 C 965 12.8 35.6 78 10 AF096393  
 C 966 12.8 35.6 79 6 ARI26057  
 C 967 12.8 35.6 80 14 MDVAD  
 C 968 12.8 35.6 81 14 AF018362  
 C 969 12.8 35.6 81 14 AF166791  
 C 970 12.8 35.6 83 6 AX240981  
 C 971 12.8 35.6 83 6 AX241021  
 C 972 12.8 35.6 84 11 AGRP25T7  
 C 973 12.8 35.6 87 10 AF041877  
 C 974 12.8 35.6 87 10 M018KCP  
 C 975 12.8 35.6 87 10 M018KCP  
 C 976 12.8 35.6 89 6 AX046263  
 C 977 12.8 35.6 89 6 AX046264  
 C 978 12.8 35.6 89 6 S77398S1  
 C 979 12.8 35.6 90 6 I49792  
 C 980 12.8 35.6 90 6 HUMABP  
 C 981 12.8 35.6 95 9 HS299561  
 C 982 12.8 35.6 96 3 AB015654  
 C 983 12.8 35.6 96 3 H0MTCRAZ  
 C 984 12.8 35.6 97 10 H010502514  
 C 985 12.8 35.6 98 6 I42296  
 C 986 12.8 35.6 98 6 HSAJ5152  
 C 987 12.8 35.6 100 6 ARI28598  
 C 988 12.8 35.6 100 6 G43568  
 C 989 12.6 33.0 20 6 AX188409  
 C 990 12.6 33.0 20 6 AX293348  
 C 991 12.6 33.0 21 6 A50871  
 C 992 12.6 33.0 21 6 ARI62021  
 C 993 12.6 33.0 21 6 AX201227  
 C 994 12.6 33.0 22 6 AX134191  
 C 995 12.6 33.0 22 11 H0M011LB  
 C 996 12.6 33.0 23 6 I49664  
 C 997 12.6 33.0 23 6 E09345  
 C 998 12.6 33.0 23 23 E09648  
 C 999 12.6 33.0 23 23 E11796  
 C1000 12.6 33.0 24 6 ARI22191

## ALIGNMENTS

RESULT 1  
 AX299123 65 bp DNA linear PAT 26-NOV-2001  
 LOCUS AX299123  
 DEFINITION Sequence 6 from Patent WO0183528.  
 ACCESSION AX299123  
 VERSION AX299123.1 GI:17129032  
 KEYWORDS  
 ORGANISM  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE  
 AUTHORS Haynes,J.R., Macklin,M.D. and Payne,L.G.  
 TITLE Nucleic acid immunization  
 JOURNAL Patent: WO 0183528-A 6 08-NOV-2001;  
 FEATURES  
 source Location/Qualifiers  
 1..65

Query Match 55.0%; Score 19.8; DB 6; Length 65;  
 Best Local Similarity 77.4%; Pred. No. 2.7e+03;  
 Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 aaagctccacatgagcagacccaagt 35  
 DB 4 AAAGCTCCACATGAGCTTAACCGAGT 34

RESULT 2  
 AX091831 34 bp DNA linear PAT 07-SEP-2000  
 LOCUS AX091831  
 DEFINITION Sequence 30 from patent US 5994524.  
 ACCESSION AX091831  
 VERSION AX091831.1 GI:10018585  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 AUTHORS Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and Yamazaki,T.  
 TITLE Polynucleotides which encode reshaped IL-8-specific antibodies and methods to produce the same  
 JOURNAL Patent: US 5994524-A 30 30-NOV-1999;  
 FEATURES  
 source Location/Qualifiers  
 1..34 /organism="unknown"

BASE COUNT 9 a 10 c 7 g 8 t  
 ORIGIN

Query Match 53.3%; Score 19.2; DB 6; Length 34;  
 Best Local Similarity 75.0%; Pred. No. 5.1e+03;  
 Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 aaagctccacatgagcagacccaagt 35  
 DB 3 AAAGCTCCACATGAGCTTAACCGAGT 34

RESULT 3  
 ARI57739 34 bp DNA linear PAT 17-OCT-2001  
 LOCUS ARI57739  
 DEFINITION Sequence 30 from patent US 6245894.  
 ACCESSION ARI57739  
 VERSION ARI57739.1 GI:16218746  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 AUTHORS Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and Yamazaki,T.  
 TITLE Reshaped human antibody to human interleukin-8  
 JOURNAL Patent: US 6245894-A 30 12-JUN-2001;  
 FEATURES  
 source Location/Qualifiers  
 1..34 /organism="unknown"

BASE COUNT 9 a 10 c 7 g 8 t  
 ORIGIN

Query Match 53.3%; Score 19.2; DB 6; Length 34;  
 Best Local Similarity 75.0%; Pred. No. 5.1e+03;  
 Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Oy 4 aaagcttcaccatgagccaggacaccaagt 35
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Db 3 AAAGCTTCACCATGAGTGTGCTCACTCAGGT 34

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[illegible]

REFERENCE	1 (bases 1 to 55)
AUTHORS	Jolly,D.J., Chang,S.M.W., Lee,W.T.L., Townsend,K. and O'Dea,J
TITLE	Hepatitis therapeutics
JOURNAL	Patent: US 6297048-A 14-02-OCT-2001;
FEATURES	Location/Qualifiers
source	1..55
BASE COUNT	25 a 16 c 6 g 8 t
ORIGIN	/organism="unknown"

Query Match	51.7%	Score 18.6;	DB 6;	Length 55;
Best Local Similarity	72.7%	Pred. No. 8.4e+03;		
Matches	24;	Conservative	0;	Mismatches 9;
			Indels	0;
			Gaps	0;

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QY      1  gcgaagcttcacccatgagccaggaaccaaa 33
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Db      3  GCCTAAGCTTCACCATGAGCACAATCTCTAA 35

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RESULT	5	55 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	BD005508				
DEFINITION	BD005508	Compositions and methods for treating intracellular diseases.			
ACCESSION	BD005508				
VERSION	BD005508.1	GI:18633879			
KEYWORDS	JP 2001500738-A/14.				
SOURCE	unidentified.				
ORGANISM	unidentified.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 55)	Salberg, M., Milich, D.R. and Lee, W.T.L.	Compositions and methods for treating intracellular diseases	Patent: JP 2001500738-A 14 23-JAN-2001;	
	CHIRON CORP, THE SCRIPPS RESEARCH INSTITUTE			OS Unidentified

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PN JP 2001500738-A/14
PD 23-JAN-2001
PE 16-SEP-1997 JP 1998514832
PR
MATI SALBERG, DAVID R MITCHELL, WILLIAM T L, IEE PC
CJ2N15/36, A61K48/00, A61K39/12, A61K39/29 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..55
/organism='Unidentified'.

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FEATURES	Location/Qualifiers
source	1..55 /organism="unidentified" /db_xref="taxon:32644"
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ORIGIN	

Query Match	51.7%;	Score 18.6;	DB 6;	Length 55;
Best Local Similarity	72.7%;	Pred. No. 8.4e+03;		

	Matches	24;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;
Oy	1	gggaagcgtccacatgagccagacacaaa	33							
	11		1111111111111111							
				1	1	1	1	1	1	1
Db	3	gcttaagcttcacacatgagacaaatcttaa	35							

RESULT	6						
AX326742		AX326742	75 bp	DNA	linear	PAT 07-JAN-2002	
LOCUS		Sequence 3	from Patent WO01/7295.				
DEFINITION		AX326742					
ACCESSION		AX326742.1	GI:18097468				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
		synthetic construct.					
		synthetic construct.					

REFERENCE	1 (sites)
AUTHORS	zander, M. and Smith, E. S.
TITLE	Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL	Patent: WO 0172935-A 3 04-OCT-2001; UNIVERSITY OF ROCHESTER (US)
FEATURES	location/Qualifiers
SOURCE	1..75

	Nucleotide Sequence of pEL/ck			
BASE COUNT	19 a	16 c	19 g	21 t
ORIGIN				

Query Match	50.6%	Score 18.2	DB 6	Length 75
Best Local Similarity	74.2%	Pred. No. 1.2e+04		
Matches 23; Conservative	0	Mismatches 8	Indels 0	Gaps 0

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QY      4  aaagctccaccatgagccaggacaccaaaag  34
          |||||  |||||  |||||  |||||  |||||
Db     40  AAAGCGCGCGCATGGGCGCGCGCCGCAACG  70

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RESULT	7				
AX275053					
LOCUS	AX275053	36 bp	DNA		
DEFINITION	Sequence 12 from Patent WO0118172.		linear		PAT 29-OCT-2001
VERSION	AX275053				
ACCESSION	AX275053.1	GI:16547657			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	LOCATION/QUALIFIERS
1 (sites)	
Euarchyrola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.	
Thomason, A.R., Liu, B. and Danilenko, D.M.	
Fibroblast growth factor-like polypeptides	
Patent: WO 0118172-A 12 15-MAR-2001.	
Amgen Inc., (US)	
	Location/Qualifiers

BASE COUNT	10 a	12 c	8 g	6 t
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"			

Query Match	50.0%	Score 18:	DB 6:	length 36:
Best Local Similarity	80.8%	Pred No.	1.6e+04:	
Matches 21; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy	2	cgaagcttcacccatgagccagac	27
Db	4	CTAAGCTTCCACCATGAGCTCGAC	29

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RESULT 8
LOCUS A63737 48 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 1 from Patent WO9723613.
ACCESSION A63737
VERSION A63737.1 GI:3717315
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 48)
AUTHORS Bebbington,C.R., Lawson,A.D., Weir,A.N. and Finney,H.M.
TITLE CELL ACTIVATION PROCESS AND REAGENTS THEREFOR
JOURNAL Patent: WO 9723613-A 1 03-JUL-1997;
JOURNAL CELTECH THERAPEUTICS LTD (GB)
COMMENT Other publication AU 120197 19970717.
FEATURES
source
location/Qualifiers
1..48
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 10 a 20 c 8 g 10 t
ORIGIN

Query Match 50.0%; Score 18; DB 6; Length 48;
Best Local Similarity 70.6%; Pred. No. 1.5e+04;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 cgaagcttcacatgagccagacccaagt 35
|||
Db 11 ccacattcgccagcagcaccacagt 44

RESULT 9
LOCUS A36805 82 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 24 from Patent EP0589840.
ACCESSION A36805
VERSION A36805.1 GI:2294071
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: EP 0589840-A 24 30-MAR-1994;
JOURNAL CTBA GEIGY AG (CH)
COMMENT Other publication JP 6225788 940816
Other publication NZ 248743 950427
Other publication CN 1088986 940706
Other publication CA 2106719 940325
Other publication AU 4748893 940331
Other publication ZA 9307033 940811
Other publication NO 933394 940325.
Other publication FI 934145 940325.
FEATURES
source
location/Qualifiers
1..82
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 11 a 23 c 23 g 25 t
ORIGIN

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Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacattgagccagacccaagt 36
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Db 60 CCACCTTCGCCAGGCGCACCAAGTG 35

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RESULT 10
LOCUS AR075883 82 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5958708.
ACCESSION AR075883
VERSION AR075883.1 GI:10002629
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: US 5958708-A 24 28-SEP-1999;
JOURNAL Location/Qualifiers
FEATURES
source
location/Qualifiers
1..82
/organism="unknown"
BASE COUNT 11 a 23 c 23 g 25 t
ORIGIN

Query Match 50.0%; Score 18; DB 6; Length 82;
Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacattgagccagacccaagt 36
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Db 60 CCACCTTCGCCAGGCGCACCAAGTG 35

RESULT 11
LOCUS AR097672 82 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6072035.
ACCESSION AR097672
VERSION AR097672.1 GI:12806402
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: US 6072035-A 24 06-JUN-2000;
JOURNAL Location/Qualifiers
FEATURES
source
location/Qualifiers
1..82
/organism="unknown"
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Query Match 50.0%; Score 18; DB 6; Length 82;
Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacattgagccagacccaagt 36
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Db 60 CCACCTTCGCCAGGCGCACCAAGTG 35

RESULT 12
LOCUS AX277694 36 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 1 from Patent WO0177681.
ACCESSION AX277694
VERSION AX277694.1 GI:16604839
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (sites)
AUTHORS Waring,R.D. and Phoenix,J.

```



FEATURES	Test-assay for diagnosis of autism and related disorders			
JOURNAL	Patent: WO 0177681-A 1 18-Oct-2001;			
SHS	International Ltd. (GB)			
source	Location/Qualifiers			
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/db_xref="taxon:32644"	/db_xref="Primer for FPST"			
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ORIGIN				
Query Match	48.9%;	Score 17.6;	DB 6;	Length 36;
Best Local Similarity	83.3%;	Pred. No. 2e+04;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
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Db	1	gggaagcttcacgactgcgctg	24	
RESULT 13				
LOCUS	AF166785/c	81 bp	RNA	linear VRL 01-SEP-1999
DEFINITION	Hepatitis C virus clone p1 polyprotein gene, partial cds.			
ACCESSION	AF166785			
VERSION	AF166785.1	GI:5814686		
KEYWORDS	Hepatitis C virus.			
SOURCE	Hepatitis C virus.			
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;			
REFERENCE	Hepatitis C virus.			
AUTHORS	1 (bases 1 to 81)			
TITLE	Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.			
JOURNAL	The genetic heterogeneity of hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha therapy			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 81)			
TITLE	Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.			
JOURNAL	Direct Submission			
FEATURES	Submitted (08-JUL-1999) Lab of Virology, Toulouse University Hospital, Place Baylac, Toulouse 31059, France			
source	Location/Qualifiers			
1. .81	/organism="Hepatitis C virus"			
/db_xref="taxon:11103"	/clone="p1"			
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/note="hypervariable region 1"	<1. .>81			
/codon_start=1	/product="polyprotein"			
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ORIGIN	21 a	21 c	20 g	19 t
Query Match	48.9%;	Score 17.6;	DB 14;	Length 81;
Best Local Similarity	83.3%;	Pred. No. 2e+04;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
Oy	8	cttcaccatgagccaagacacca	31	
Db	41	ctggcaccatgagccatggcacca	18	
RESULT 14				
AF166788/c				

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LOCUS       AF166788                81 bp    RNA      linear   VRL_01-SEP-1999
DEFINITION  Hepatitis C virus clone p19 polypeptide gene, partial cds.
ACCESSION   AF166788
VERSION     AF166788.1  GI:5814689
KEYWORDS
SOURCE      ORGANISM              Hepatitis C virus.
               Hepatitis C virus
               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Hepacivirus.
REFERENCE   1  (bases 1 to 81)
AUTHORS    Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.
TITLE      The genetic heterogeneity of hypervariable region 1 of the viral
           genome and the sensitivity of hepatitis C virus to interferon alpha
           therapy
JOURNAL    Unpublished
REFERENCE   2  (bases 1 to 81)
AUTHORS    Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.
TITLE      Direct Submission
JOURNAL    Submitted (08-JUL-1999) Lab of Virology, Toulouse University
           Hospital, Place Baylac, Toulouse 31059, France
FEATURES             Location/Qualifiers
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Best Local Similarity 83.3%; Pred. NO. 2e+04;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      8 ctccaccatgagccagacaacca 31
Db      41 CTGGCACCATGAGCCATGGCACCA 18

RESULT 15
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LOCUS       AF166792
DEFINITION  Hepatitis C virus clone P3 polypeptide gene, partial cds.
ACCESSION   AF166792
VERSION     AF166792.1  GI:5814693
KEYWORDS
SOURCE      ORGANISM              Hepatitis C virus.
               Hepatitis C virus
               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Hepacivirus.
REFERENCE   1  (bases 1 to 81)
AUTHORS    Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.
TITLE      The genetic heterogeneity of hypervariable region 1 of the viral
           genome and the sensitivity of hepatitis C virus to interferon alpha
           therapy
JOURNAL    Unpublished
REFERENCE   2  (bases 1 to 81)
AUTHORS    Sandres,K., Dubois,M., Pasquier,C. and Izopet,J.
TITLE      Direct Submission
JOURNAL    Submitted (08-JUL-1999) Lab of Virology, Toulouse University
           Hospital, Place Baylac, Toulouse 31059, France
FEATURES             Location/Qualifiers
     source          1..81
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 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 ctccaccatgagccagcacca 31  
 || ||||| ||||| |||||  
 Db 41 CTGCAACCATGAGCATGCA 18

Search completed: June 22, 2002, 05:31:51  
 Job time: 5071 sec

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:15:25 ; Search time 369.89 Seconds  
(without alignments)  
167.101 Million cell updates/sec

Title: US-09-927-267-12

Perfect score: 36

Sequence: 1 gcgaagctccacatgagccagcaccacaagt 36

## Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 2046006

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.8	55.0	65	24	AA170936 Influenza virus M2
2	19.2	53.3	34	17	AA116940 Murine anti-human
3	18.6	51.7	38	17	AA098659 Human neurotensin
4	18.6	51.7	55	14	AA047027 HCV core sequence
5	18.6	51.7	55	19	AAV30020 PCR primer used to
6	18.6	51.7	55	22	AA021201 Sense PCR primer #
7	18.2	50.6	75	21	AA152323 Nucleotide sequenc
8	18.2	50.6	75	22	AA01475 Partial pEL/tk seq
9	18	50.0	36	22	AA00786 Human fibroblast G

10	18	50.0	48	18	AA090515 Human CPM1 antibo
11	18	50.0	53	19	AA041509 Nucleotide sequenc
12	18	50.0	82	15	AA044724 Oligonucleotide us
13	18	50.0	82	20	AA228558 Oligonucleotide C2
14	17.6	48.9	31	22	AA130004 Human single nucle
15	17.6	48.9	36	24	ABA95305 Human tyrosyl prot
16	17.6	48.9	41	21	AA092074 Porcine Lhx3 PCR p
17	17.4	48.3	33	20	AA091346 Oligonucleotide LA
18	17.4	48.3	41	18	AA069228 Human B7-1 primer
19	17	47.2	43	14	AA049777 PCR primer for amp
20	17	47.2	75	21	AA02076 Porcine Lhx3 PCR p
21	17	47.2	96	18	AA065270 Platelet derived g
22	17	47.2	96	20	AA087057 Staphylococcus aur
23	16.8	46.7	31	16	AA076298 primer used in pre
24	16.8	46.7	35	20	AAV04356 primer for amplify
25	16.8	46.7	35	20	AAV83185 Murine OPg PCR pri
26	16.8	46.7	35	22	AA057758 Neurexin victoria
27	16.8	46.7	45	18	AA075700 Primer for amplify
28	16.8	46.7	45	20	AA080458 Human silent SNP c
29	16.6	46.1	51	22	AA174029 Human silent SNP c
30	16.6	46.1	51	22	AA179219 Human silent SNP c
31	16.6	46.1	51	22	AA179219 Human secreted pro
32	16.6	46.1	96	21	AA012460 IL-6R antibody pri
33	16.4	45.6	35	13	AA031338 Secretory componen
34	16.4	45.6	46	17	AA130860 TGF-beta1 5' PCR p
35	16.2	45.0	29	14	AA041608 Alpha-v beta-3 Mab
36	16.2	45.0	33	20	AA071829 Human pronf-alpha
37	16.2	45.0	37	16	AA080247 Human transport pr
38	16.2	45.0	51	21	AA076384 Human transport pr
39	16.2	45.0	51	21	AA076386 Human SNP oligonuc
40	16.2	45.0	51	22	AA033366 Chimeric antibody
41	16.2	45.0	63	21	AA032763 Alpha-v beta-3 Mab
42	16.2	45.0	90	20	AA071827 IL-6R antibody pri
43	16.2	45.0	98	20	AA071819 PCR primer for inh
44	16	44.4	36	13	AA031346 PCR primer for colla
45	16	44.4	37	14	AA037720 PCR primer for 24k-Fex
46	16	44.4	37	19	AA023119 PCR primer used to
47	16	44.4	37	19	AA016246 Lepomis centrarchi
48	16	44.4	38	22	AA168137 Beta-actin targett
49	16	44.4	47	22	AA011917 Nucleotide sequenc
50	16	44.4	69	21	AA015232 Partial p7.5/tk se
51	16	44.4	69	22	AA040147 T cell receptor V
52	15.8	43.9	33	20	AA023512 Human p53 cDNA pri
53	15.8	43.9	36	16	AA097853 Human p53 PCR prim
54	15.8	43.9	36	21	AA061638 Murine osteoproteg
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56	15.8	43.9	56	19	AAV70302 T. brucei trypanos
57	15.6	43.3	34	16	AA052888 Primers for constru
58	15.6	43.3	38	21	AA012115 Human osteogen re
59	15.6	43.3	39	22	AA056705 Mercuric ion reduc
60	15.6	43.3	40	21	AA063496 Primer 549-563N to
61	15.6	43.3	40	22	AA075098 T. brucei trypanos
62	15.6	43.3	52	20	AA028603 Human genomic DNA
63	15.6	43.3	72	24	AA02790 Murine FGF-like CD
64	15.6	43.3	83	21	AA012138 Murine anti-body ON
65	15.6	43.3	83	21	AA012138 Humanised anti-HM1
66	15.4	42.8	34	19	AAV39375 PCR primer used in con
67	15.4	42.8	34	22	AA014974 PCR primer for DNA
68	15.4	42.8	37	22	AA000784 Murine fibroblast
69	15.4	42.8	37	22	AA089362 Human kinase codin
70	15.4	42.8	51	22	AA089362 Human kinase codin
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80	15.4	42.8	51	22	AA089362 Human kinase codin
81	15.2	42.2	70	21	AA013231 Inducible nitric o
82	15.2	42.2	20	20	AA034343 Human Inducible n

C	83	15.2	42.2	20	21	AAA33787	Low adenosine anti
C	84	15.2	42.2	24	22	AAAF32536	Escherichia coli r
C	85	15.2	42.2	28	15	AAQ61792	Sequence of 5'-3'
C	86	15.2	42.2	28	18	AAFS5636	Human prostaglandi
C	87	15.2	42.2	28	22	AAFS58439	Human hocii clone
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C	89	15.2	42.2	30	21	AAA96776	PCR primer for his
C	90	15.2	42.2	30	21	AAA96788	PCR primer for his
C	91	15.2	42.2	33	12	AAQ11051	Part of JUN305 enc
C	92	15.2	42.2	37	22	AAH96772	Human Chk1 ribozym
C	93	15.2	42.2	37	23	ABK05398	Human NCOG G-Cleav
C	94	15.2	42.2	50	22	AAK34597	Human SNP oligonuc
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C	99	15.2	42.2	51	22	AAH40632	Human SNP flanking
C	100	15.2	42.2	54	22	AAAD18180	Linker peptide enc
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C	102	15	41.7	17	20	AAK00121	Human antibody PCR
C	103	15	41.7	17	21	AAZ58901	PCR primer MBCLIVS
C	104	15	41.7	17	22	AAH75094	Nucleotide sequenc
C	105	15	41.7	17	22	AAH74273	Nucleotide sequenc
C	106	15	41.7	17	22	AAH76632	Humanised anti-PTH
C	107	15	41.7	17	22	AAE68117	Human L chain V re
C	108	15	41.7	17	22	AAE69173	Human L chain V re
C	109	15	41.7	17	22	AAE69229	Human L chain V re
C	110	15	41.7	23	22	AAE98150	Human IGEBRA gene P
C	111	15	41.7	24	18	AAE80258	Oligo HCV88, target
C	112	15	41.7	26	22	AAH37466	SNP specific lower
C	113	15	41.7	31	19	AAV24250	Chimeric antibody
C	114	15	41.7	31	20	AAK00094	Mouse humanised an
C	115	15	41.7	31	21	AAZ58875	PCR primer MBC-SI.
C	116	15	41.7	31	22	AAH75068	PCR primer used in
C	117	15	41.7	31	22	AAH74249	PCR primer used in
C	118	15	41.7	31	22	AAH76606	Mouse Ig VH PCR pr
C	119	15	41.7	31	22	AAE68091	Chimeric antibody
C	120	15	41.7	31	22	AAE68147	Chimeric antibody
C	121	15	41.7	31	22	AAE69203	Chimeric antibody
C	122	15	41.7	32	21	AAA92428	MBL-1 L chain V r
C	123	15	41.7	32	22	AAH78134	PCR primer used to
C	124	15	41.7	32	22	ABAA4509	PCR primer MLS. S
C	125	15	41.7	34	18	AAE73598	Primer used in pre
C	126	15	41.7	34	18	AAE73600	Primer used in pre
C	127	15	41.7	34	19	AAV39136	Primer 5 for agein
C	128	15	41.7	36	13	AAQ31344	II-6R antibody pri
C	129	15	41.7	37	17	AAI16941	Murine anti-human
C	130	15	41.7	38	22	AAE29734	Human alpha,2-man
C	131	15	41.7	39	16	AAO79003	Poliiovirus nucleot
C	132	15	41.7	40	18	AAE93608	Eosinophil total R
C	133	15	41.7	41	17	AAE738312	Human B-cell trans
C	134	15	41.7	41	19	AAV32205	Human B-cell trans
C	135	15	41.7	41	21	AAZ90100	PCR primer used to
C	136	15	41.7	41	22	AAO93300	Human B-cell trans
C	137	15	41.7	42	17	AAE05838	Primer for haemato
C	138	15	41.7	43	16	AAO94488	Murine antibody ON
C	139	15	41.7	43	17	AAE73603	Chimaeric human/mu
C	140	15	41.7	44	15	AAQ68639	A33 heavy chain va
C	141	15	41.7	44	16	AAO80382	Mouse light chain
C	142	15	41.7	44	16	AAO80449	L243 VL region 5'
C	143	15	41.7	44	17	AAO73999	Mab 39D10 light ch
C	144	15	41.7	50	22	AAH89647	Human kinase codin
C	145	15	41.7	51	22	AAI33101	Human SNP oligonuc
C	146	15	41.7	51	22	AAI74028	Human silent SNP c
C	147	15	41.7	51	22	AAI75106	Human silent SNP c
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C	150	15	41.7	51	22	AAI75109	Human silent SNP c
C	151	15	41.7	64	13	AAQ33617	Upstream sequence
C	152	15	41.7	86	14	AAQ36807	Mycobacterium 16S
C	153	15	41.7	96	21	AAAC11237	Human secreted pro
C	154	14.8	41.1	26	15	AAO67138	Junction site sequ
C	155	14.8	41.1	26	20	AAK27786	Sequence of juncti
C	156	14.8	41.1	30	15	AAQ58501	Sequence of primer
C	157	14.8	41.1	36	20	AAK21835	Primer EB18748 for
C	158	14.8	41.1	36	22	AAE92283	LRBI gene knockou
C	159	14.8	41.1	37	22	AAH96741	Human Chk1 ribozym
C	160	14.8	41.1	38	20	AAZ24695	CD3delta cDNA frag
C	161	14.8	41.1	41	22	AAH20045	M. intracellulare
C	162	14.8	41.1	41	22	AAH20046	M. intracellulare
C	163	14.8	41.1	43	18	AAH20046	Glycine heavy chain
C	164	14.8	41.1	43	19	AAV39271	Primer O-532 used
C	165	14.8	41.1	43	20	AAZ23025	Oligonucleotide us
C	166	14.8	41.1	50	22	AAI28495	Human SNP oligonuc
C	167	14.8	41.1	51	22	AAE73685	Human transport pr
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C	171	14.8	41.1	62	22	AAAD21200	Antisense PCR prim
C	172	14.6	40.6	21	19	AAZ26480	Human polymorphic
C	173	14.6	40.6	21	22	AAI1094	Bacterial 16S RNA
C	174	14.6	40.6	27	18	AAV70436	Human KDR VEGF rec
C	175	14.6	40.6	28	20	AAV59858	Mutagenic oligonuc
C	176	14.6	40.6	31	18	AAE62463	Granule bound star
C	177	14.6	40.6	31	19	AAV12108	Human Fas ligand c
C	178	14.6	40.6	32	22	AAE65095	Murine SKIP PCR pr
C	179	14.6	40.6	34	21	AAAI4964	PCR primer for DNA
C	180	14.6	40.6	35	21	AAAG90137	PCR primer for del
C	181	14.6	40.6	37	21	AAQ80242	Rat proNDF-alpha2c
C	182	14.6	40.6	37	16	AAE64922	Rat motif I #18740
C	183	14.6	40.6	38	22	AAE75414	Codon-optimised HP
C	184	14.6	40.6	39	17	AAE75414	Topoisomerase-I f
C	185	14.6	40.6	48	22	AAE75414	PCR primer p132 to
C	186	14.6	40.6	50	22	AAI18159	Human silent SNP c
C	187	14.6	40.6	51	21	AAI78024	Human transport pr
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C	190	14.6	40.6	51	22	AAI78383	Human silent SNP c
C	191	14.6	40.6	51	22	AAH39796	Human SNP flanking
C	192	14.6	40.6	56	21	AAZ58962	Primer for constru
C	193	14.6	40.6	57	21	AAZ29452	PCR primer T131, t
C	194	14.6	40.6	58	20	AAK07081	Human KDS1 protein
C	195	14.6	40.6	60	19	AAV21321	Immunoglobulin I m
C	196	14.6	40.6	61	17	AAE34881	GRE expression pla
C	197	14.6	40.6	75	23	AAE49574	Staphylococcus aur
C	198	14.6	40.6	86	17	AAE88594	Staphylococcus aur
C	199	14.6	40.6	87	23	AAE49917	Staphylococcus aur
C	200	14.6	40.6	87	23	AAE49925	Human foetal liver
C	201	14.6	40.6	95	22	ABAT2378	Probe #16651 for g
C	202	14.6	40.6	95	22	ABAT38185	Human brain expres
C	203	14.6	40.6	95	22	AAK20803	Human bone marrow
C	204	14.6	40.6	95	22	AAK46953	Human bone marrow
C	205	14.6	40.6	95	22	AAI25792	Probe #15725 for g
C	206	14.6	40.6	95	22	AAI25790	Probe #21476 used
C	207	14.6	40.6	100	22	AAI4700	Human brain expres
C	208	14.6	40.6	100	22	AAI46474	Probe #15160 used
C	209	14.4	40.0	20	17	AAI16966	Human/murine chima
C	210	14.4	40.0	20	17	AAI16966	5' Mutagenic prime
C	211	14.4	40.0	24	22	AAI69973	Human peroxidosome
C	212	14.4	40.0	27	21	AAAB7591	Rat hepatocyte car
C	213	14.4	40.0	30	19	AAV24270	Chimeric antibody
C	214	14.4	40.0	30	20	AAK00114	Human antibody PCR
C	215	14.4	40.0	30	21	AAZ58895	PCR primer MBCLIVS
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C	217	14.4	40.0	30	22	AAH74267	Nucleotide sequenc
C	218	14.4	40.0	30	22	AAH76626	Humanised anti-PTH
C	219	14.4	40.0	30	22	AAAF69111	Human H chain V re
C	220	14.4	40.0	30	22	AAAF69167	Human H chain V re
C	221	14.4	40.0	30	22	AAE69223	Human H chain V re
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C	223	14.4	40.0	32	17	AAE39757	Human mucosal add
C	224	14.4	40.0	32	18	AAV35277	PCR primer HUMDIG
C	225	14.4	40.0	32	19	AAV20094	PCR primer used to
C	226	14.4	40.0	32	22	AAH24014	Tobacco plastid 16
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C	228	14.4	40.0	34	18	AAE94641	Human FGF-10 plasm

C	229	14.4	40.0	34	19	AAV68229	Human cytoctatin I	302	14.2	39.4	51	22	AAI78206	Human silent SNP c	
	230	14.4	40.0	34	19	AAV51357	Human TRID PCR pri	303	14.2	39.4	51	22	AAI78208	Human silent SNP c	
	231	14.4	40.0	34	12	AAV90783	Human RMR-5 (TRID	304	14.2	39.4	51	22	AAI78210	Human silent SNP c	
	232	14.4	40.0	36	13	AAO31339	IL-6R antibody pri	305	14.2	39.4	51	22	AAI78211	Human silent SNP c	
	233	14.4	40.0	36	19	AAV24252	Chimeric antibody	306	14.2	39.4	51	22	AAH39500	Human SNP flanking	
	234	14.4	40.0	36	20	AAK00096	Mouse humanised an	307	14.2	39.4	51	22	AAH40676	Human SNP flanking	
	235	14.4	40.0	36	21	AAZ58877	PCR primer MBCHWS	C	308	14.2	39.4	60	21	AAA29521	Codon altered alka
	236	14.4	40.0	36	22	AAH75070	PCR primer used to	309	14.2	39.4	68	21	AAA29521	Human secreted pro	
	237	14.4	40.0	36	22	AAH74251	Nucleotide sequenc	C	310	14.2	39.4	71	15	AAO70457	PCR primer to amplify
	238	14.4	40.0	36	22	AAH76508	Human Ig VH PCR pr	311	14.2	39.4	76	21	AAA65575	PCR primer used to	
	239	14.4	40.0	36	22	AAE69093	Chimeric antibody	C	312	14.2	39.4	86	21	AAC13117	Human secreted pro
	240	14.4	40.0	36	22	AAE69149	Chimeric antibody	313	14.2	39.4	87	16	AAO82768	3'-5' oligo 4 for	
	241	14.4	40.0	36	22	AAE69205	Chimeric antibody	314	14.2	39.4	87	22	AAE73725	HGF nucleic acid 1	
	242	14.4	40.0	37	21	AAV33690	Bacteriophage lamb	C	315	14.2	39.4	90	22	ABA49394	Human breast cell
	243	14.4	40.0	37	21	AAZ64925	RPI motif I #18750	C	316	14.2	39.4	90	22	ABA67304	Human foetal liver
	244	14.4	40.0	40	21	AAA94219	Drosophila Na+ dri	C	317	14.2	39.4	90	22	ABA34398	Probe #12864 for g
	245	14.4	40.0	41	20	AAK56286	Human TAB1 PCR pri	C	318	14.2	39.4	90	22	AAK15741	Human brain expres
	246	14.4	40.0	41	21	AAK60281	Human HPC2 CDNA ex	C	319	14.2	39.4	90	22	AAK41478	Human bone marrow
	247	14.4	40.0	41	24	AAK59016	Human prostate can	C	320	14.2	39.4	90	22	AAI22226	Probe #12159 for g
	248	14.4	40.0	42	18	AAAT9085	Elastase specific	C	321	14.2	39.4	90	22	AAI47521	Probe #16207 used
	249	14.4	40.0	45	14	AAO48347	Mab 25D2 light cha	C	322	14.2	39.4	90	22	AAI07924	Probe #7915 used t
	250	14.4	40.0	45	16	AAO98855	Anti-human IL-4 hu	C	323	14.2	39.4	92	22	ABA70477	Human foetal liver
	251	14.4	40.0	45	24	ABA94307	Mouse cloaked-2 CD	C	324	14.2	39.4	92	22	AAK18722	Human brain expres
	252	14.4	40.0	51	21	AAAT7158	Human clone c94394	C	325	14.2	39.4	92	22	AAK44635	Human bone marrow
	253	14.4	40.0	51	22	AAI27273	Human SNP oligonuc	C	326	14.2	39.4	92	22	AAI50635	Probe #19321 used
	C	254	14.4	51	22	AAI75841	Human silent SNP c	C	327	14.2	39.4	94	20	AAK62101	Fragment of the nu
	C	255	14.4	51	22	AAK505276	Mouse ES cell nucl	C	328	14.2	39.4	96	14	AAO47829	BMP cDNA. Homo sa
	256	14.4	40.0	53	20	AAV54312	Primer JMWCR13 use	C	329	14.2	39.4	99	22	AAK82677	Human mature BMP e
	257	14.4	40.0	53	20	AAV55394	Soluble sc-TCR fus	C	330	14.2	38.9	19	21	AAK27771	5' Mutagenic prime
	258	14.4	40.0	55	15	AAQ56579	5'-primer to const	C	331	14.2	38.9	23	20	AAK90511	MP13* transgene P
	C	259	14.4	57	17	AAAT58925	Rabbit gastric lip	C	332	14.2	38.9	25	16	AAO94537	PCR primer RHP 1.
	C	260	14.4	59	22	ABA01485	PCR primer MM439.	C	333	14.2	38.9	25	17	AAAT8651	Chimeric human/mu
	C	261	14.4	60	16	AAAT00232	Thrombin 60N DNA 1	C	334	14.2	38.9	25	19	AAV39394	Humanised anti-HM1
	C	262	14.4	60	22	AAAT00784	Thrombin high affi	C	335	14.2	38.9	25	18	AAK59443	Primer used in con
	263	14.4	40.0	63	21	AAZ32754	Chimeric antibody	C	336	14.2	38.9	27	18	AAK67295	Human fil1 VEGF re
	C	264	14.4	66	19	AAV60663	Rabbit gastric lip	C	337	14.2	38.9	27	18	AAK74458	Mouse fil-1 VEGF r
	265	14.4	40.0	68	22	AAAF8097	Translation initia	C	338	14.2	38.9	27	18	AAK74227	Mouse fil-1 VEGF r
	266	14.4	40.0	68	22	AAAF89710	Nucleotide sequenc	C	339	14.2	38.9	27	18	AAK70727	Human KDR VEGF rec
	267	14.4	40.0	69	21	AAZ88084	Nuclear lacZ gene	C	340	14.2	38.9	29	21	AAZ47517	PCR primer bar-1 f
	268	14.4	40.0	72	20	AAZ32800	Reshaped f19 light	C	341	14.2	38.9	31	22	AAAF61403	Substrate vector p
	C	269	14.4	74	14	AAO48342	Mab 25D2 light cha	C	342	14.2	38.9	31	22	AAAF61408	Human acth PCR pri
	C	270	14.4	74	16	AAO98851	Anti-human IL-4 hu	C	343	14.2	38.9	32	21	AAAF94229	MAB-1 H chain V r
	C	271	14.4	89	19	AAV40067	PCR primer S9 from	C	344	14.2	38.9	32	24	AAH78135	PCR primer used to
	272	14.4	40.0	98	22	AAK32537	PCR primer Seq ID	C	345	14.2	38.9	33	24	ABA04510	PCR primer MHS. S
	C	273	14.4	98	20	AAK32538	PCR primer Seq ID	C	346	14.2	38.9	32	24	ABA04561	PCR primer #31. S
	C	274	14.4	99	21	AAK51471	Oligonucleotide la	C	347	14.2	38.9	32	24	ABA04570	PCR primer #33. S
	275	14.4	40.0	99	22	ABA72565	Human foetal liver	C	348	14.2	38.9	33	13	AAO31131	Probe 100 specific
	276	14.4	40.0	99	22	AAK20992	Human brain expres	C	349	14.2	38.9	33	14	AAQ46437	Hepatitis C virus
	277	14.4	40.0	99	22	AAK47144	Human bone marrow	C	350	14.2	38.9	33	17	AAAT34644	Primer for creatin
	278	14.4	40.0	99	22	AAI52979	Probe #21665 used	C	351	14.2	38.9	33	18	AAAT60487	Calbindin 5' PCR p
	279	14.2	39.4	23	18	AAAT60464	WSP PCR primer P3	C	352	14.2	38.9	33	20	AAK23726	Human killer adria
	280	14.2	39.4	25	22	AAH39499	SNP specific SNPE	C	353	14.2	38.9	34	19	AAV39376	Humanised anti-HM1
	C	281	14.2	27	19	AAV98458	Human EGF-R hamer	C	354	14.2	38.9	34	20	AAK59426	Primer used in con
	282	14.2	39.4	29	20	AAK30770	Forward PCR primer	C	355	14.2	38.9	34	21	AAAF57817	Primer used to amp
	283	14.2	39.4	29	22	AAH91297	Human inflammatory	C	356	14.2	38.9	35	19	AAV24264	Chimeric antibody
	284	14.2	39.4	30	21	AAZ93075	Primer used to gen	C	357	14.2	38.9	35	20	AAK23725	Human killer adria
	C	285	14.2	32	15	AAO88809	BoPCar I, bovine p	C	358	14.2	38.9	35	20	AAK00108	Human antibody PCR
	286	14.2	39.4	36	20	AAK55287	Human ZAP-70 codin	C	359	14.2	38.9	35	21	AAZ58889	PCR primer MBCHL1
	287	14.2	39.4	38	20	AAK08501	Murine VH primer.	C	360	14.2	38.9	35	22	AAH75082	Nucleotide sequenc
	288	14.2	39.4	40	19	AAV32209	Human B-cell trans	C	361	14.2	38.9	35	22	AAH74261	Nucleotide sequenc
	289	14.2	39.4	40	21	AAZ90104	PCR primer used in	C	362	14.2	38.9	35	22	AAH76620	Chimeric anti-PNtr
	290	14.2	39.4	40	22	AAAD9304	Human B-cell trans	C	363	14.2	38.9	35	22	AAH21269	Human Kv4.2 associ
	C	291	14.2	44	21	AAZ58220	Arabidopsis phosph	C	364	14.2	38.9	35	22	AAAF69105	Chimeric antibody
	C	292	14.2	45	21	AAA53222	Human G-protein co	C	365	14.2	38.9	35	22	AAAF69161	Chimeric antibody
	293	14.2	39.4	46	20	AAK29222	DEL19736551 primer	C	366	14.2	38.9	35	22	AAAF69217	Chimeric antibody
	C	294	14.2	50	22	AAK30918	Human SNP oligonuc	C	367	14.2	38.9	37	17	AAAT10948	Human/murine chiMa
	295	14.2	39.4	50	22	AAAL34619	Human SNP oligonuc	C	368	14.2	38.9	37	22	AAAL14962	PCR primer for DNA
	296	14.2	39.4	50	22	AAAL34620	Human SNP oligonuc	C	369	14.2	38.9	37	22	AAH96764	Human Chk1 ribozym
	297	14.2	39.4	51	21	AAAF76328	Human Ig heavy cha	C	370	14.2	38.9	38	19	AAV36094	PCR primer used fo
	298	14.2	39.4	51	21	AAAF76329	Human Ig heavy cha	C	371	14.2	38.9	38	21	AAZ60685	PCR primer used to
	C	299	14.2	51	22	AAAL33119	Human SNP oligonuc	C	372	14.2	38.9	38	22	AAAD20139	Human tatarotene-l
	C	300	14.2	51	22	AAAT75334	Human silent SNP c	C	373	14.2	38.9	39	18	AAAT13836	Heliothis ecdysona
	301	14.2	39.4	51	22	AAAT78204	Human silent SNP c	C	374	14.2	38.9	40	17	AAAT88662	VEGF nucleic acid

375	14	38.9	40	22	AA511916	Capture nucleic ac	c 448	13.8	38.3	51	22	AAH89363	Human kinase codin
376	14	38.9	40	22	AA511921	Competitor oligon	c 449	13.8	38.3	51	22	AAH89365	Human kinase codin
377	14	38.9	40	22	AA511921	Capture oligonucle	c 450	13.8	38.3	51	22	AAH89361	Human kinase codin
378	14	38.9	40	22	AA511921	Beta-actin capture	c 451	13.8	38.3	51	22	AAH90363	Human clone cg4398
379	14	38.9	40	22	AA511921	Beta-actin capture	c 452	13.8	38.3	51	22	AAH90363	Human clone cg4398
380	14	38.9	41	18	AA511921	2E12 sfv PCR prime	c 453	13.8	38.3	51	22	AAH40012	Human SNP flanking
381	14	38.9	41	20	AA511921	2E12 sfv PCR prime	c 454	13.8	38.3	51	22	AAH40012	Human SNP flanking
382	14	38.9	41	20	AA511921	Duplex forming oli	c 455	13.8	38.3	54	22	AA511921	Human SNP flanking
383	14	38.9	42	19	AA511921	C-Jun amino acids	c 456	13.8	38.3	55	14	AA511921	Interleukin-11 co
384	14	38.9	43	24	AA511921	Histamine H4 recep	c 457	13.8	38.3	55	14	AA511921	Ig gamma4 CHI regl
385	14	38.9	45	21	AA511921	Human ICAW-1 DNA f	c 458	13.8	38.3	57	21	AA511921	Human interleukin-
386	14	38.9	47	21	AA511921	Human map-related	c 459	13.8	38.3	58	21	AA511921	Formula I oligonuc
387	14	38.9	47	23	AA511921	CNS disorder-relat	c 460	13.8	38.3	60	16	AA511921	Fc-gamma-R-RIIa cyt
388	14	38.9	50	22	AA511921	Human kinase codin	c 461	13.8	38.3	60	19	AA511921	Immunoglobulin genom
389	14	38.9	50	22	AA511921	Human kinase codin	c 462	13.8	38.3	60	22	AA511921	Mouse Fc-gamma-RII
390	14	38.9	51	21	AA511921	Human ribosomal pr	c 463	13.8	38.3	64	21	AA511921	Mouse Fc-gamma-RII
391	14	38.9	51	22	AA511921	Human SNP oligonuc	c 464	13.8	38.3	70	24	AA511921	Primer #19 for int
392	14	38.9	51	22	AA511921	Human silent SNP c	c 465	13.8	38.3	73	22	AA511921	Human MLH1 (bMLH1)
393	14	38.9	51	22	AA511921	Human clone cg4394	c 466	13.8	38.3	75	22	AA511921	Human immune/haema
394	14	38.9	54	12	AA511921	Leader sequence of	c 467	13.8	38.3	80	14	AA511921	B subunit p53 p53 ge
395	14	38.9	54	13	AA511921	Oligonucleotide du	c 468	13.8	38.3	80	16	AA511921	MAB 25D2 light cha
396	14	38.9	54	15	AA511921	Lysozyme gene synt	c 469	13.8	38.3	80	16	AA511921	Anti-human IL-4 hu
397	14	38.9	56	20	AA511921	Junction site betw	c 470	13.8	38.3	85	16	AA511921	PADRE-Influenza ma
398	14	38.9	56	20	AA511921	Ubiquitin maize pr	c 471	13.8	38.3	85	16	AA511921	Human gene signatu
399	14	38.9	57	18	AA511921	Staphylococcus aur	c 472	13.8	38.3	86	21	AA511921	Chimeric receptor
400	14	38.9	57	21	AA511921	Human secreted pro	c 473	13.8	38.3	86	21	AA511921	Oligonucleotide A8
401	14	38.9	63	21	AA511921	Human secreted pro	c 474	13.8	38.3	86	22	AA511921	Human breast cance
402	14	38.9	65	21	AA511921	Human secreted pro	c 475	13.8	38.3	86	22	AA511921	Oligonucleotide fo
403	14	38.9	71	21	AA511921	Human secreted pro	c 476	13.8	38.3	86	22	AA511921	Human primary sign
404	14	38.9	75	22	AA511921	Human breast cell	c 477	13.8	38.3	87	22	AA511921	Chimeric receptor
405	14	38.9	75	22	AA511921	Human foetal liver	c 478	13.8	38.3	87	21	AA511921	Oligonucleotide A8
406	14	38.9	75	22	AA511921	Probe #1156 for g	c 479	13.8	38.3	87	21	AA511921	Human secreted pro
407	14	38.9	75	22	AA511921	Human bone marrow	c 480	13.8	38.3	87	21	AA511921	Human breast cance
408	14	38.9	75	22	AA511921	Human bone marrow	c 481	13.8	38.3	87	22	AA511921	Human breast cance
409	14	38.9	75	22	AA511921	Probe #10492 for g	c 482	13.8	38.3	87	22	AA511921	Oligonucleotide fo
410	14	38.9	75	22	AA511921	Probe #14455 used t	c 483	13.8	38.3	87	22	AA511921	Human primary sign
411	14	38.9	75	22	AA511921	Probe #6249 used t	c 484	13.8	38.3	87	22	AA511921	Chimeric receptor
412	14	38.9	79	21	AA511921	Human secreted pro	c 485	13.8	38.3	87	22	AA511921	Oligonucleotide A8
413	14	38.9	81	17	AA511921	VEGF nucleic acid	c 486	13.8	38.3	100	15	AA511921	Human primary sign
414	14	38.9	90	13	AA511921	93 mer of human be	c 487	13.8	38.3	20	22	AA511921	Hepatitis A virus
415	14	38.9	93	13	AA511921	Fragment of the nu	c 488	13.8	38.3	20	22	AA511921	Rat PTP1B antisens
416	14	38.9	94	20	AA511921	Human foetal liver	c 489	13.8	38.3	21	22	AA511921	PCR generated 16S
417	14	38.9	100	22	AA511921	Probe #17370 for g	c 490	13.8	38.3	21	22	AA511921	Duplex forming oli
418	14	38.9	100	22	AA511921	Human brain expres	c 491	13.8	38.3	24	20	AA511921	Human gene single
419	14	38.9	100	22	AA511921	Human bone marrow	c 492	13.8	38.3	24	20	AA511921	PCR primer #8 used
420	14	38.9	100	22	AA511921	Probe #16125 for g	c 493	13.8	38.3	25	21	AA511921	primer KRTTM-Nest-
421	14	38.9	100	22	AA511921	Probe #22806 used	c 494	13.8	38.3	27	19	AA511921	Neurofibromatosis
422	14	38.9	100	22	AA511921	Mouse flk-1 VEGF r	c 495	13.8	38.3	27	19	AA511921	Matze rin26 RNA pr
423	14	38.9	100	22	AA511921	Mouse flk-1 VEGF r	c 496	13.8	38.3	28	21	AA511921	Human EGF-R hamper
424	14	38.9	100	22	AA511921	Human KDR VEGF rec	c 497	13.8	38.3	28	21	AA511921	Oligonucleotide C
425	14	38.9	100	22	AA511921	Human KDR VEGF rec	c 498	13.8	38.3	28	22	AA511921	PCR primer for mur
426	14	38.9	100	22	AA511921	Human KDR VEGF re	c 499	13.8	38.3	28	22	AA511921	Oligonucleotide C:
427	14	38.9	100	22	AA511921	Primer used in RT/	c 500	13.8	38.3	28	22	AA511921	Oligonucleotide C.
428	14	38.9	100	22	AA511921	Primer 1 for human	c 501	13.8	38.3	29	21	AA511921	Polymorphic fragme
429	14	38.9	100	22	AA511921	Mouse Tumour necro	c 502	13.8	38.3	31	18	AA511921	Granule bound star
430	14	38.9	100	22	AA511921	Human single nucle	c 503	13.8	38.3	31	18	AA511921	Granule bound star
431	14	38.9	100	22	AA511921	Primer FMB5 used t	c 504	13.8	38.3	31	18	AA511921	Granule bound star
432	14	38.9	100	22	AA511921	Keratinocyte growt	c 505	13.8	38.3	32	17	AA511921	Bacterialum nitrored
433	14	38.9	100	22	AA511921	Human keratinocyte	c 506	13.8	38.3	33	21	AA511921	Probe A used in th
434	14	38.9	100	22	AA511921	Human B-cell trans	c 507	13.8	38.3	33	22	AA511921	Probe A used in ol
435	14	38.9	100	22	AA511921	MT-MMP-5 polypepti	c 508	13.8	38.3	33	22	AA511921	Oligonucleotide pr
436	14	38.9	100	22	AA511921	Chimeric DDAD JK-9	c 509	13.8	38.3	33	22	AA511921	Probe A: SEQ ID 1.
437	14	38.9	100	22	AA511921	Human Chk1 ribozym	c 510	13.8	38.3	33	22	AA511921	Synthetic probe A.
438	14	38.9	100	22	AA511921	Hepatitis GB virus	c 511	13.8	38.3	34	12	AA511921	Self paired oligon
439	14	38.9	100	22	AA511921	HBV gene hybridis	c 512	13.8	38.3	34	12	AA511921	tpa primer 5 for t
440	14	38.9	100	22	AA511921	Human TGF-beta ant	c 513	13.8	38.3	35	20	AA511921	Tissue plasminogen
441	14	38.9	100	22	AA511921	PCR primer P17 for	c 514	13.8	38.3	35	20	AA511921	PCR primer used to
442	14	38.9	100	22	AA511921	Pichia pastoris ge	c 515	13.8	38.3	36	16	AA511921	tfl DNA polymerase
443	14	38.9	100	22	AA511921	P64 PCR primer, to	c 516	13.8	38.3	36	21	AA511921	Synthetic oligonuc
444	14	38.9	100	22	AA511921	Human T-cell recep	c 517	13.8	38.3	36	21	AA511921	Plasmid pCGN8620 o
445	14	38.9	100	22	AA511921	Human T-cell recep	c 518	13.8	38.3	36	21	AA511921	Oligo used in plan
446	14	38.9	100	22	AA511921	M. tuberculosis 16	c 519	13.8	38.3	36	21	AA511921	Arabidopsis ALDH c
447	14	38.9	100	22	AA511921	Test sequence from	c 520	13.8	38.3	36	22	AA511921	Plant expression v

C 521	13.6	37.8	36	22	AAE24480	Human ICE coding s	C 594	13.6	37.8	84	21	AAZ34759	Anti-CD23 C11 huma
522	13.6	37.8	36	24	AAAS6948	Plasmid pCGN8620 o	595	13.6	37.8	84	22	ABA72455	Human foetal liver
523	13.6	37.8	37	22	AAH96699	Human Chk1 ribozym	596	13.6	37.8	84	22	ABA38227	Probe #16693 for g
C 524	13.6	37.8	37	22	AAE30239	Beta-actin primer	597	13.6	37.8	84	22	AAK20878	Human brain expres
C 525	13.6	37.8	37	22	AAE30240	Beta-actin strain	598	13.6	37.8	84	22	AAK47031	Human bone marrow
C 526	13.6	37.8	37	22	AAE30253	Beta-actin sequenc	599	13.6	37.8	84	22	AAI25814	Probe #15747 for g
C 527	13.6	37.8	37	23	ABK05445	Human NCOG G-Cleav	600	13.6	37.8	84	22	AAI52867	Probe #21553 used
528	13.6	37.8	37	23	ABK08456	Human CD20 G-Cleav	601	13.6	37.8	85	21	AAA36671	RSV and PIV fusion
529	13.6	37.8	38	21	AAAG0283	Human HPC2 CDNA ex	C 602	13.6	37.8	86	22	AAI26156	Human breast cance
530	13.6	37.8	38	24	AAAS9018	Human prostate can	C 603	13.6	37.8	90	22	AAI49908	Human transporter-
C 531	13.6	37.8	39	16	AAQ97482	A. actinomycetemco	604	13.6	37.8	91	22	ABA69691	Human foetal liver
C 532	13.6	37.8	39	22	AAAS1198	Beta-actin targett	605	13.6	37.8	97	22	ABA70672	Human foetal liver
C 533	13.6	37.8	39	22	AAH23597	E coli ATP synthas	606	13.6	37.8	97	22	AAK18918	Human brain expres
534	13.6	37.8	40	19	AAV21004	PCR primer p85-top	607	13.6	37.8	97	22	AAK44863	Human bone marrow
C 535	13.6	37.8	41	19	AAV24253	Chimeric antibody	C 608	13.6	37.8	97	22	AAI50839	Human bone marrow
C 536	13.6	37.8	41	20	AAK00097	Mouse humanised an	C 609	13.6	37.8	99	22	AAI05823	Probe #19525 used
C 537	13.6	37.8	41	21	AAZ58878	PCR primer MBCLHR	C 610	13.6	37.8	99	22	AAI05823	Human reproductive
C 538	13.6	37.8	41	21	AAH75071	PCR primer used to	C 611	13.4	37.2	15	22	AAI05824	Human reproductive
C 539	13.6	37.8	41	22	AAH74997	PCR primer used to	C 612	13.4	37.2	24	15	AAE52082	IGF-1 oligonucleot
C 540	13.6	37.8	41	22	AAH74252	Nucleotide sequenc	C 613	13.4	37.2	25	22	AAH77502	cbhl-Phytase prime
C 541	13.6	37.8	41	22	AAH76609	Human Ig VH PCR pr	C 614	13.4	37.2	27	18	AAK73905	Human DNA repair p
C 542	13.6	37.8	41	22	AAE69094	Chimeric antibody	C 615	13.4	37.2	27	18	AAK73905	Mouse flt-1 VEGF r
C 543	13.6	37.8	41	22	AAE69150	Chimeric antibody	C 616	13.4	37.2	27	18	AAK67736	Human fltl VEGF r
C 544	13.6	37.8	41	22	AAE69206	Chimeric antibody	617	13.4	37.2	28	15	AAO68879	Primer exon 1 for
C 545	13.6	37.8	41	22	AAE69206	Human Nucleotide 1	618	13.4	37.2	28	21	AAZ46009	Self paired oligon
C 546	13.6	37.8	42	21	AAZ48326	Primer specific fo	C 619	13.4	37.2	29	19	AAE68773	Downstream PCR pri
C 547	13.6	37.8	42	22	AAH46385	KISS-1 Oligomer #3	C 620	13.4	37.2	29	19	AAE68773	Human secreted pro
C 548	13.6	37.8	42	22	AAH46389	KISS-1 Oligomer #7	621	13.4	37.2	29	19	AAE68773	Murine AGP-1 PCR p
549	13.6	37.8	44	22	AAH18929	Human CLASP-1 Intr	622	13.4	37.2	30	14	AAO32890	Cytomegalovirus ta
550	13.6	37.8	44	12	AAO12691	Rel light chain va	C 623	13.4	37.2	30	21	AAAV19127	Human toll-like re
C 551	13.6	37.8	45	22	AAE57426	C. pneumoniae lpdA	624	13.4	37.2	33	21	AAAV7542	Metabotropic gluta
C 552	13.6	37.8	45	22	AAE25920	Ceramide affinity	625	13.4	37.2	33	21	AAV37782	PCR primer for CDN
C 553	13.6	37.8	47	21	AAZ65384	Human map-related	626	13.4	37.2	34	15	AAO68880	Human TNFR-6 alpha
C 554	13.6	37.8	48	20	AAK08564	Oligonucleotide fr	627	13.4	37.2	34	17	AAI18376	Self paired oligon
C 555	13.6	37.8	50	18	AAV79434	Staphylococcus aur	628	13.4	37.2	34	17	AAI18376	Primer #2 for c1b
556	13.6	37.8	50	23	ABL00250	Human silent nonco	629	13.4	37.2	34	22	AAE31200	Oligonucleotide 5C
557	13.6	37.8	51	22	AAI29548	Human SNP oligonuc	630	13.4	37.2	37	21	AAZ39523	Human corpuscles o
558	13.6	37.8	51	22	AAI74469	Human silent SNP c	631	13.4	37.2	37	22	AAE83303	Human corpuscles o
559	13.6	37.8	51	22	AAI74471	Human silent SNP c	632	13.4	37.2	37	22	AAE83303	Human staminaloccl
560	13.6	37.8	51	22	AAI74948	Human silent SNP c	633	13.4	37.2	41	18	AAE97209	Corpuscles of Stan
C 561	13.6	37.8	51	22	AAI76013	Human silent SNP c	C 634	13.4	37.2	42	20	AAK32428	Kappa chain variab
C 562	13.6	37.8	51	22	AAI77139	Human silent SNP c	635	13.4	37.2	44	20	AAK32428	scfv 10F6 heavy ch
563	13.6	37.8	51	22	AAI78324	Human silent SNP c	636	13.4	37.2	44	22	AAE6997	Probe used to Isol
564	13.6	37.8	51	22	AAH79831	Human DNA containi	637	13.4	37.2	44	19	AAE6997	Human PRO polyonucl
565	13.6	37.8	51	22	AAH79831	Human DNA containi	638	13.4	37.2	45	19	AAE6997	Restriction fragme
C 566	13.6	37.8	51	22	AAH79831	Human SNP flanking	639	13.4	37.2	45	22	AAE6997	Human prostate CDN
C 567	13.6	37.8	51	23	ABL000759	Human silent nonco	640	13.4	37.2	45	22	AAE6997	Human prostate CDN
568	13.6	37.8	56	15	AAO67104	Human amino acid c	641	13.4	37.2	45	22	AAH3876	P703P epitope enco
C 569	13.6	37.8	58	16	AAI21603	Mutagenic primer M	642	13.4	37.2	46	21	AAH3876	P703P epitope enco
570	13.6	37.8	60	8	AAI21603	Human gene signatu	C 643	13.4	37.2	48	19	AAV99849	PCR primer used to
571	13.6	37.8	60	19	AAV65642	phthalphal-3 alpha-	C 644	13.4	37.2	48	20	AAV99849	Spinalia oleracea
572	13.6	37.8	63	8	AAI21603	Target sequence us	645	13.4	37.2	50	22	AAI33752	M. intracellulare
573	13.6	37.8	65	16	AAI24893	Human gene signatu	C 646	13.4	37.2	50	22	AAI33752	Human SNP oligonuc
C 574	13.6	37.8	68	19	AAV65658	Oligonucleotide us	C 647	13.4	37.2	51	22	AAI74588	Human SNP oligonuc
C 575	13.6	37.8	68	19	AAV65659	Oligonucleotide us	648	13.4	37.2	51	22	AAI75614	Human silent SNP c
C 576	13.6	37.8	72	14	AAQ34670	DNA encoding hcg b	C 649	13.4	37.2	51	22	AAH39596	Human SNP flanking
C 577	13.6	37.8	72	20	AAZ37460	Oligo 596 for hcg	650	13.4	37.2	58	16	AAO67528	CMV enhancer/promo
C 578	13.6	37.8	74	22	AAZ32962	DNA encoding CARDI	651	13.4	37.2	60	19	AAV48316	Nucleotide sequenc
579	13.6	37.8	80	16	AAI62783	C-reactive protein	652	13.4	37.2	60	21	AAZ45704	Primer for Bacillu
C 580	13.6	37.8	80	17	AAI88622	VEGF nucleic acid	C 653	13.4	37.2	60	22	AAI88622	Porcine factor VII
C 581	13.6	37.8	80	17	AAI71618	C-terminal coding	654	13.4	37.2	66	22	AAO44754	Synthetic gene shp
582	13.6	37.8	80	20	AAK66657	CDNA encoding a pe	655	13.4	37.2	68	18	AAO77227	Fibroblast growth
C 583	13.6	37.8	80	20	AAK33789	Bacillus sp. GUS g	656	13.4	37.2	69	15	AAO56771	Murine WAP-human p
C 584	13.6	37.8	80	20	AAK60073	DNA encoding CRP M	657	13.4	37.2	70	22	AAH77310	IGC Fab-BPI fusion
C 585	13.6	37.8	80	21	AAAI99781	Secretabale microbl	C 658	13.4	37.2	74	16	AAO33033	Sequence encoding
586	13.6	37.8	80	21	AAAI99781	Human C-reactive p	659	13.4	37.2	78	19	AAV48326	Nucleotide sequenc
587	13.6	37.8	81	16	AAI62782	C-reactive protein	C 660	13.4	37.2	80	22	AAV48326	C. utillis crty prt
588	13.6	37.8	81	16	AAI62782	CDNA encoding a pe	C 661	13.4	37.2	80	22	ABA48613	Human breast cell
589	13.6	37.8	81	20	AAK66658	CDNA encoding a pe	C 662	13.4	37.2	80	22	ABA66524	Human foetal liver
590	13.6	37.8	81	20	AAK6072	DNA encoding CRP f	C 663	13.4	37.2	80	22	ABA33588	Probe #12054 for g
591	13.6	37.8	81	20	AAK6072	DNA encoding CRP f	C 664	13.4	37.2	80	22	AAK14948	Human brain expres
592	13.6	37.8	81	21	AAAI2234	Human C-reactive p	C 665	13.4	37.2	80	22	AAK14948	Human bone marrow
593	13.6	37.8	81	21	AAAI2236	Human C-reactive p	C 666	13.4	37.2	80	22	AAI46734	Probe #15420 used

C 667	13.4	37.2	80	22	AAI07140	Probe #7131 used t	740	13.2	36.7	41	20	AAV79896	RNA ligand sequenc
C 668	13.4	37.2	81	18	AAQ38894	glti variable domai	741	13.2	36.7	41	21	AAV92996	High-affinity nucl
C 669	13.4	37.2	81	14	AAT85870	CCR-grafted light	742	13.2	36.7	41	22	AAH20044	M. intracellulare
C 670	13.4	37.2	81	21	AAZ46946	glt2 variable domai	743	13.2	36.7	41	22	AAAC84467	Oligo used in cons
C 671	13.4	37.2	86	21	AAAC66477	Chimeric receptor	744	13.2	36.7	44	16	AAO881535	Primer for the hum
C 672	13.4	37.2	86	21	AAAC68005	Oligonucleotide A8	745	13.2	36.7	44	22	AAAC90792	Gag-pol PCR primer
C 673	13.4	37.2	86	22	AAAL19495	Human breast cance	746	13.2	36.7	44	22	AAAC92925	Gag-pol PCR primer
C 674	13.4	37.2	86	22	AAAH24851	Oligonucleotide fo	747	13.2	36.7	45	18	AAT96943	Mooney MLV gag-po
C 675	13.4	37.2	86	22	AAH24434	Human primary sign	748	13.2	36.7	45	18	AAT96943	Primer for Moloney
C 676	13.4	37.2	86	22	AAH24506	Human primary sign	749	13.2	36.7	45	18	AAV27927	hcaLR3 5'probe. S
C 677	13.4	37.2	87	21	AAAC66479	Chimeric receptor	750	13.2	36.7	45	21	AAA07315	PCR primer for PST
C 678	13.4	37.2	87	21	AAAC68007	Oligonucleotide A8	751	13.2	36.7	45	22	AAAS11876	Synthetic cdna enc
C 679	13.4	37.2	87	22	AAAH24853	Oligonucleotide fo	752	13.2	36.7	46	22	AAAF56162	Rat FAS cdna mutag
C 680	13.4	37.2	87	22	AAAH24436	Human primary sign	753	13.2	36.7	46	22	AAAF56163	Rat FAS cdna mutag
C 681	13.4	37.2	87	22	AAAH24508	Human primary sign	754	13.2	36.7	46	22	AAAF56164	Rat FAS cdna mutag
C 682	13.4	37.2	89	20	AAAX32526	Betaliphal/CW-2 a	755	13.2	36.7	46	22	AAAF56165	Rat FAS cdna mutag
C 683	13.4	37.2	92	16	AAT22075	Human gene signal	756	13.2	36.7	46	22	AAAF56166	Rat FAS cdna mutag
C 684	13.4	37.2	92	22	AAAS24731	Human ovarian PCR-	757	13.2	36.7	46	22	AAAF56167	Rat FAS cdna mutag
C 685	13.4	37.2	94	24	ABK17273	Coupled ligation a	758	13.2	36.7	47	20	AAV81528	Oligonucleotide us
C 686	13.4	37.2	94	24	ABK17274	Coupled ligation a	759	13.2	36.7	48	13	AAQ24671	PCR primer XH for
C 687	13.4	37.2	94	24	ABK17298	Coupled ligation a	760	13.2	36.7	48	14	AAQ36598	PCR primer XH for
C 688	13.4	37.2	94	24	ABK17311	Coupled ligation a	761	13.2	36.7	48	14	AAQ35196	CAMPATH-1H heavy c
C 689	13.4	37.2	96	13	AAO33516	Upstream sequence	762	13.2	36.7	48	14	AAQ43766	Sequence of primer
C 690	13.4	37.2	96	22	AAAF80155	Nucleotide sequence	763	13.2	36.7	48	21	AAAC61603	PCR primer used to
C 691	13.4	37.2	100	22	ABAT74350	Human foetal liver	764	13.2	36.7	48	21	AAAT73045	Transglutaminase r
C 692	13.4	37.2	100	22	ABAT39271	Probe #17737 for g	765	13.2	36.7	48	21	AAZ34768	Human Igcl constan
C 693	13.4	37.2	100	22	ABAL19692	Human breast cance	766	13.2	36.7	49	17	AAT06517	Protein antigen b
C 694	13.4	37.2	100	22	AAK22816	Human brain expres	767	13.2	36.7	49	17	AAT06517	Human antigen b
C 695	13.4	37.2	100	22	AAK48987	Human bone marrow	768	13.2	36.7	50	22	AAAT28867	Human SNP oligonuc
C 696	13.4	37.2	100	22	AAI26398	Probe #16331 for g	769	13.2	36.7	50	22	AAAL34621	Human SNP oligonuc
C 697	13.4	37.2	100	22	AAI54815	Probe #23501 used	770	13.2	36.7	50	22	AAAF76766	T flavus promoter
C 698	13.2	36.7	18	15	AAO63237	PCR primer for amp	771	13.2	36.7	50	22	ABAI0696	Tall adaptor oligo
C 699	13.2	36.7	19	18	AAT80253	Oligo HCV59, targe	772	13.2	36.7	51	16	AAV25038	Human gene signal
C 700	13.2	36.7	19	21	AAAH84585	Cyclin E ribozyme	773	13.2	36.7	51	19	AAV23733	PCR primer used in
C 701	13.2	36.7	19	22	AAH59747	Cyclin E ribozyme	774	13.2	36.7	51	22	AAAL27485	Human SNP oligonuc
C 702	13.2	36.7	20	14	AAO35073	HCV envelope regio	775	13.2	36.7	51	22	AAAL28413	Human SNP oligonuc
C 703	13.2	36.7	20	22	AAAF72363	PCR primer specifi	776	13.2	36.7	51	22	AAAL28628	Human SNP oligonuc
C 704	13.2	36.7	20	22	AAAF23221	Oligonucleotide fo	777	13.2	36.7	51	22	AAAL29532	Human SNP oligonuc
C 705	13.2	36.7	20	22	AAAF23656	Human PPARgamma an	778	13.2	36.7	51	22	AAAL33408	Human SNP oligonuc
C 706	13.2	36.7	20	22	AAAF23657	Human PPARgamma an	779	13.2	36.7	51	22	AAAT73293	Human silent SNP c
C 707	13.2	36.7	20	22	AAAC65549	Human focal adhesi	780	13.2	36.7	51	22	AAAT75885	Human silent SNP c
C 708	13.2	36.7	20	24	AAAS15397	Human focal adhesi	781	13.2	36.7	51	22	AAAT78202	Human silent SNP c
C 709	13.2	36.7	24	18	AAV00196	Human insulin PCR	782	13.2	36.7	51	22	AAAT78665	Human silent SNP c
C 710	13.2	36.7	27	17	AAT12656	5' primer for CTGF	783	13.2	36.7	51	22	AAAT79022	Human silent SNP c
C 711	13.2	36.7	27	18	AAAH67768	Human IL1I VEGF re	784	13.2	36.7	51	22	AAAT79566	Human silent SNP c
C 712	13.2	36.7	27	19	AAV98300	Human EGF-R hamme	785	13.2	36.7	51	22	AAAT79567	Human silent SNP c
C 713	13.2	36.7	27	19	AAV94480	Canine IL-2 recept	786	13.2	36.7	51	22	AAH89382	Human structural p
C 714	13.2	36.7	27	20	AAZ11723	Human CTGF-2 5' PC	787	13.2	36.7	51	22	AAH89383	Human structural p
C 715	13.2	36.7	27	22	AAAH43358	TNF-alpha (antisen	788	13.2	36.7	51	23	ABL00321	Human silent nonco
C 716	13.2	36.7	30	13	AAQ31387	IL-6R antibody pri	789	13.2	36.7	52	22	AAAD06896	Human Oligo 3 to c
C 717	13.2	36.7	30	22	AAAF77642	A thaliana enhance	790	13.2	36.7	56	21	AAAS52403	Tdt-expressing lam
C 718	13.2	36.7	31	22	AAAS04545	Gene expression pr	791	13.2	36.7	57	5	AAVA0217	Gene encoding lead
C 719	13.2	36.7	31	22	AAAS07247	G protein-coupled	792	13.2	36.7	58	15	AAO65621	C-terminal primer
C 720	13.2	36.7	32	21	AAZ877002	Mouse ERG9 DNA amp	793	13.2	36.7	58	20	AAZ22735	3' primer for porc
C 721	13.2	36.7	33	22	AAH79001	Human nuclear tran	794	13.2	36.7	58	20	AAV64812	Zona pellucida zp
C 722	13.2	36.7	33	22	AAAF77833	Human Cdk4-Irg2 cni	795	13.2	36.7	58	21	AAZ95672	Porcine ZPC PCR pr
C 723	13.2	36.7	33	22	AAAF56399	Linker oligonucleo	796	13.2	36.7	58	21	AAZ46280	Porcine ZPC PCR pr
C 724	13.2	36.7	36	22	AAZ36935	PCR primer used to	797	13.2	36.7	58	21	AAZ33269	Recombinant porc



C 813	13.2	36.7	67	21	AA023154	Human secreted pro	C 886	13	36.1	27	18	AA070792	Human KDR VEGF rec
C 814	13.2	36.7	67	20	AA018510	RNA polymerase I c	C 887	13	36.1	27	19	AA094182	Mouse IL-2 recepto
C 815	13.2	36.7	69	24	AA034332	Lysosyme signal pe	C 888	13	36.1	27	19	AA05756	Probe used to isol
C 816	13.2	36.7	74	22	AA093134	Human HIV/tumorige	C 889	13	36.1	28	21	AA049246	HCV core protein p
C 817	13.2	36.7	74	22	AA094553	Genetic suppressor	C 890	13	36.1	28	21	AA046148	Plasmid pghCV/delt
C 818	13.2	36.7	79	22	AA076529	Human foetal liver	C 891	13	36.1	30	13	AA027056	HCV primer p27. S
C 819	13.2	36.7	79	22	AA041040	Probe #19506 for g	C 892	13	36.1	30	13	AA031815	Lambda gtl PCR pr
C 820	13.2	36.7	79	22	AA025167	Human brain expres	C 893	13	36.1	30	14	AA050510	Primer for heparit
C 821	13.2	36.7	79	22	AA051173	Human bone marrow	C 894	13	36.1	30	20	AA028374	PCR primer for hum
C 822	13.2	36.7	79	22	AA028181	Probe #18114 for g	C 895	13	36.1	30	22	AA017444	PCR primer used to
C 823	13.2	36.7	79	22	AA0157223	Probe #25909 used	C 896	13	36.1	31	18	AA016447	Amilase gene PCR p
C 824	13.2	36.7	81	12	AA011240	Encodes feline Ieu	C 897	13	36.1	31	21	AA061601	PCR primer used to
C 825	13.2	36.7	82	20	AA089813	Seq ID No: 13 of W	C 898	13	36.1	31	22	AA0129547	Human single nucle
C 826	13.2	36.7	82	20	AA089811	Synthetic human op	C 899	13	36.1	32	22	AA020869	TSHR extracellular
C 827	13.2	36.7	82	20	AA089812	Human foetal liver	C 900	13	36.1	33	24	AA017220	Coupled ligation a
C 828	13.2	36.7	82	22	AA074506	Probe #17804 for g	C 901	13	36.1	34	15	AA069173	PCR primer LDGF 10
C 829	13.2	36.7	82	22	AA039338	Human brain expres	C 902	13	36.1	35	13	AA020992	R1U primer 3 for T
C 830	13.2	36.7	82	22	AA022975	Human bone marrow	C 903	13	36.1	36	17	AA0134112	Humanised 2B6 anti
C 831	13.2	36.7	82	22	AA049149	Human bone marrow	C 904	13	36.1	36	19	AA021729	p53 CDNA RT-PCR pr
C 832	13.2	36.7	82	22	AA054981	Probe #23667 used	C 905	13	36.1	36	19	AA010882	Human MLH1 gene PC
C 833	13.2	36.7	84	22	AA069024	Human immune/haema	C 906	13	36.1	36	19	AA003507	HEM humanised hea
C 834	13.2	36.7	84	22	AA069663	Human immune/haema	C 907	13	36.1	37	23	AA005375	Human NCOG G-Cleav
C 835	13.2	36.7	84	22	AA069664	Human immune/haema	C 908	13	36.1	37	23	AA005377	Human NCOG G-Cleav
C 836	13.2	36.7	86	18	AA065250	Platelet derived g	C 909	13	36.1	38	14	AA048005	PCR primer for V k
C 837	13.2	36.7	86	20	AA087034	Human brain expres	C 910	13	36.1	38	21	AA033773	Invertase specific
C 838	13.2	36.7	87	22	AA020384	Human bone marrow	C 911	13	36.1	38	22	AA041034	PCR primer for met
C 839	13.2	36.7	87	22	AA046490	Human breast cell	C 912	13	36.1	39	17	AA008955	Primer FV94-2864R
C 840	13.2	36.7	88	22	AA048547	Human foetal liver	C 913	13	36.1	39	19	AA066276	Primer FV94-2864R
C 841	13.2	36.7	88	22	AA066459	Human foetal liver	C 914	13	36.1	39	19	AA058454	Primer OMRSD2-34
C 842	13.2	36.7	88	22	AA033519	Probe #11985 for g	C 915	13	36.1	39	19	AA059922	Sense primer OMRbs
C 843	13.2	36.7	88	22	AA0414878	Human bone marrow	C 916	13	36.1	39	19	AA056239	HGV primer FV94-28
C 844	13.2	36.7	88	22	AA040612	Human bone marrow	C 917	13	36.1	39	20	AA081954	S. putrefaciens OR
C 845	13.2	36.7	88	22	AA0121377	Probe #11310 for g	C 918	13	36.1	39	20	AA016502	PCR primer used to
C 846	13.2	36.7	88	22	AA046658	Probe #15344 used	C 919	13	36.1	39	20	AA025514	US556134 Seq ID 2
C 847	13.2	36.7	88	22	AA0107072	Probe #7063 used t	C 920	13	36.1	39	20	AA082245	Heptellits G virus
C 848	13.2	36.7	89	14	AA037001	Proinsulin oligonu	C 921	13	36.1	39	21	AA011547	S. putrefaciens P
C 849	13.2	36.7	90	22	AA040314	Probe #18760 for g	C 922	13	36.1	41	16	AA094070	p3reverse4(P3R4) p
C 850	13.2	36.7	91	19	AA020453	Human c-src oncog	C 923	13	36.1	41	22	AA077099	Human ATP-dependen
C 851	13.2	36.7	93	21	AA017942	Human secreted pro	C 924	13	36.1	42	13	AA032268	Mutagenesis PCR pr
C 852	13.2	36.7	93	21	AA036672	RSV and p1V fusion	C 925	13	36.1	42	16	AA086682	Human NF-AT transcrip
C 853	13.2	36.7	95	19	AA073239	C. utilis crtZ, p1I	C 926	13	36.1	42	21	AA029288	Human nuclear facc
C 854	13.2	36.7	97	14	AA036996	Proinsulin oligonu	C 927	13	36.1	42	21	AA026590	T cell antigen rec
C 855	13.2	36.7	97	22	AA074483	Human foetal liver	C 928	13	36.1	42	22	AA015229	Human protein C de
C 856	13.2	36.7	97	22	AA022950	Human brain expres	C 929	13	36.1	42	22	AA026367	DNA encoding human
C 857	13.2	36.7	97	22	AA049124	Human bone marrow	C 930	13	36.1	42	22	AA041849	Human protein C de
C 858	13.2	36.7	97	22	AA054954	Probe #23640 used	C 931	13	36.1	42	22	AA031700	Human NF-AT polynu
C 859	13.2	36.7	98	21	AA014718	Aspergillus oryzae	C 932	13	36.1	42	22	AA083316	Primer PC001b. SY
C 860	13.2	36.7	98	22	AA047522	Human breast cell	C 933	13	36.1	42	24	AA018772	PCR primer #13 use
C 861	13.2	36.7	98	22	AA065413	Human foetal liver	C 934	13	36.1	43	21	AA075875	PCR primer for DNA
C 862	13.2	36.7	98	22	AA039565	Human bone marrow	C 935	13	36.1	45	19	AA059383	Humanised anti-HM1
C 863	13.2	36.7	98	22	AA020375	Probe #10308 for g	C 936	13	36.1	45	20	AA059433	Primer used in con
C 864	13.2	36.7	98	22	AA045580	Probe #14266 used	C 937	13	36.1	45	22	AA082184	Human retrovirus D
C 865	13.2	36.7	98	22	AA0106077	Probe #6068 used t	C 938	13	36.1	46	13	AA031687	PCR primer for cdn
C 866	13	36.1	20	22	AA080897	PCR primer #2 for	C 939	13	36.1	46	17	AA038553	Sheep DHICys prim
C 867	13	36.1	21	18	AA076646	Mevlonate pyropho	C 940	13	36.1	47	21	AA0265935	Ovine cell adhesio
C 868	13	36.1	21	20	AA055184	Multiple antisense	C 941	13	36.1	48	15	AA073460	Human map-related
C 869	13	36.1	21	21	AA020753	Human multiple tar	C 942	13	36.1	48	19	AA017209	Egr-1 nuclear loca
C 870	13	36.1	21	21	AA021456	Human multiple tar	C 943	13	36.1	49	20	AA033649	Thrombomodulin sig
C 871	13	36.1	21	21	AA0344631	Human adenosine re	C 944	13	36.1	50	21	AA075543	Expression cassett
C 872	13	36.1	21	22	AA018163	Enhanced green flu	C 945	13	36.1	50	21	AA057783	PCR primer for cdn
C 873	13	36.1	22	22	AA044408	SPINK5 gene sequen	C 946	13	36.1	51	18	AA079399	Human TNFR-6 alpha
C 874	13	36.1	24	21	AA094036	Reverse PCR primer	C 947	13	36.1	51	21	AA077150	Staphylococcus aur
C 875	13	36.1	24	21	AA027231	Reverse PCR primer	C 948	13	36.1	51	21	AA077200	Human clone cg4394
C 876	13	36.1	24	24	AA030352	Engrailed mRNA PCR	C 949	13	36.1	51	22	AA017279	Human clone cg4395
C 877	13	36.1	24	24	AA0167719	Homeodomain transc	C 950	13	36.1	51	22	AA013367	Human SNP oligonuc
C 878	13	36.1	24	24	AA0183350	Capture oligonucle	C 951	13	36.1	51	22	AA0173288	Human silent SNP c
C 879	13	36.1	24	24	AA0183351	Capture oligonucle	C 952	13	36.1	51	22	AA0173290	Human silent SNP c
C 880	13	36.1	25	14	AA034354	Downstream PCR pri	C 953	13	36.1	51	22	AA0173292	Human silent SNP c
C 881	13	36.1	25	14	AA041717	Consensus eukaryot	C 954	13	36.1	51	22	AA0175343	Human silent SNP c
C 882	13	36.1	25	14	AA037109	Consensus eukaryot	C 955	13	36.1	51	22	AA017764	Human silent SNP c
C 883	13	36.1	26	18	AA097455	Variant Hsr gene H	C 956	13	36.1	51	22	AA0178249	Human silent SNP c
C 884	13	36.1	27	18	AA072225	Mouse flk-1 VEGF r	C 957	13	36.1	51	22	AA0178822	Human silent SNP c
C 885	13	36.1	27	18	AA071884	Mouse flk-1 VEGF r	C 958	13	36.1	51	22	AA090515	Human clone cg4394

C 959	13	36.1	51	22	AAH40628	Human SNP flanking
C 960	13	36.1	51	23	ABL00083	Human silent nonco
C 961	13	36.1	51	23	ABL00778	Human amino acid c
C 962	13	36.1	53	21	AAZ58956	Primer for constru
C 963	13	36.1	54	16	AAO95955	Signal sequence fo
C 964	13	36.1	55	18	AAT93324	Primer #1 for glyc
C 965	13	36.1	59	18	AAV79360	Staphylococcus aur
C 966	13	36.1	61	21	AAA89748	Mouse ECD-PD fusio
C 967	13	36.1	64	16	AAQ97219	Modified hlt-3 sig
C 968	13	36.1	64	16	AAT99298	Modified sequence
C 969	13	36.1	64	21	AAA03763	Modified human int
C 970	13	36.1	65	16	AAQ99612	Mouse Ah receptor
C 971	13	36.1	65	18	AAT85446	5' primer UL-68 am
C 972	13	36.1	65	19	AAV54301	Primer JMTCR2 used
C 973	13	36.1	65	20	AAZ55383	Soluble sc-TCR fus
C 974	13	36.1	66	20	AAZ77738	Human CONVL1 oligo
C 975	13	36.1	66	20	AAZ76096	Light chain consen
C 976	13	36.1	70	22	AAZ00077	Human Interferon b
C 977	13	36.1	70	22	AAZ29243	Ligand to CD40 lig
C 978	13	36.1	71	15	AAQ57942	Hepatitis A virus
C 979	13	36.1	72	13	AAQ33954	Downstream sequenc
C 980	13	36.1	72	20	AAZ59220	PCR primer CR508 u
C 981	13	36.1	73	19	AAV55420	Interleukin-3 sign
C 982	13	36.1	73	20	AAZ59218	PCR primer CR503 u
C 983	13	36.1	74	21	AAZ52804	MB83 heavy chain
C 984	13	36.1	75	15	AAQ55730	DNA ligase Oligo A
C 985	13	36.1	75	17	AAT14927	Oligo A template f
C 986	13	36.1	75	20	AAZ77739	Human CONVL1 oligo
C 987	13	36.1	75	20	AAZ76097	Light chain consen
C 988	13	36.1	76	14	AAQ49814	IL-3 signal sequen
C 989	13	36.1	77	22	ABA73545	Human foetal liver
C 990	13	36.1	77	22	ABA38820	Probe #17286 for g
C 991	13	36.1	77	22	SAK21991	Human brain expres
C 992	13	36.1	77	22	AAK48154	Human bone marrow
C 993	13	36.1	77	22	AAT26143	Probe #16076 for g
C 994	13	36.1	77	22	AAI53984	Probe #22670 used
C 995	13	36.1	79	22	AAZ43708	Cornedosomesin sin
C 996	13	36.1	81	22	AAK45635	Human bone marrow
C 997	13	36.1	81	22	AAI51566	Probe #20252 used
C 998	13	36.1	83	22	ABA70427	Human foetal liver
C 999	13	36.1	83	22	ABA71599	Human foetal liver
C1000	13	36.1	83	22	ABA37076	Probe #15542 for g

## ALIGNMENTS

## RESULT 1

ID AAT70936 standard; DNA; 65 BP.

XX	AAI70936;	
AC	12-MAR-2002 (first entry)	
XX		
DT	Influenza virus M2 antigen 5' PCR primer.	
XX		
DE	Vaccine: M2 protein; antigen; nucleic acid immunisation; Cpg;	
XX	adjuvant; PCR primer; ss.	
KW		
XX	Influenza virus type A.	
OS	Synthetic.	
OS		
XX	WO200183528-A2.	
PN		
XX	08-NOV-2001.	
PD		
XX	01-MAY-2001; 2001WO-GB01924.	
PF		
XX	01-MAY-2000; 2000US-200968P.	
PR	01-MAY-2000; 2000US-0561951.	
PR	08-JUN-2000; 2000US-210580P.	
PI		
XX		

PA (POWD-) POWDERJECT VACCINES INC.  
 PA (POWD-) POWDERJECT RES LTD.  
 XX  
 PI Haynes JR, Macklin MD, Payne LG;  
 XX WPI: 2002-041480/05.  
 DR  
 XX  
 XX  
 PT Use of nucleic acid sequence which encodes influenza virus M2 antigen  
 PT and which is not present in a recombinant viral vector, for manufacture  
 PT of medicament for vaccination against an influenza virus -  
 XX  
 PS Example 1; Page 37; 69pp; English.  
 XX  
 XX The present sequence is that of a 5' PCR primer (3' primer given  
 CC on AAT70937) used in the PCR amplification of DNA encoding the  
 CC M2 antigen of influenza virus strain A/Sydney/5/97 (H3N2). In  
 CC addition to M2-derived sequences, the 5' primer contains additional  
 CC 5' sequences that include a recognition site for HindIII and a Kozak  
 CC consensus sequence to facilitate mRNA translation initiation. The  
 CC PCR product was used in the construction of vaccine vector plasmid  
 CC PM2-FL (see AAT70939). A claimed polynucleotide vaccine  
 CC composition comprises a nucleic acid sequence that encodes the M2  
 CC antigen (see AAM50534-36) of a type A influenza virus, and which is  
 CC not present in a recombinant viral vector. Upon introduction  
 CC to a subject, the nucleic acid sequence is expressed to provide the  
 CC influenza virus M2 antigen in an amount sufficient to elicit an  
 CC immune response.  
 XX  
 SO Sequence 65 BP; 20 A; 20 C; 14 G; 11 T; 0 other;

Query Match 55.0%; Score 19.8; DB 24; Length 65;  
 Best Local Similarity 77.4%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 5 aagcttcacccatgagccagacccaagt 35  
 ||||||||||||||||| ||| | |  
 Db 4 aagcttcacccatgagcccttaaccgaggt 34

## RESULT 2

ID AAT16940 standard; DNA; 34 BP.

XX	AAT16940;	
AC	19-SEP-1996 (first entry)	
XX		
DT	Murine anti-human IL-8 MAB light V region cDNA PCR primer cHVL.	
XX		
DE	Variable; light chain; WS4; hybridoma; monoclonal; pUC-WS4-VL;	
XX	antibody; MAB; BALB/c mouse; spleen cell; human; interleukin-8;	
KW	IL-8; myeloma p3X63-Ag8.653 cell; CDR; framework; chimeric	
KW	complementarity determining region; chimeric; murine; PCR;	
KW	inflammation; disease; mediated; low antigenicity; primer;	
KW	polymerase chain reaction; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO9602576-A1.	
PD	01-FEB-1996.	
XX		
XX	12-JUL-1995; 95WO-JP01396.	
PF		
XX	14-DEC-1994; 94JP-0310785.	
PR	13-JUL-1994; 94JP-0161481.	
PR	24-NOV-1994; 94JP-0289951.	
XX		
PA	(CHUS ) CHUGAI SEIYAKU KK.	
XX		
XX	Matsumoto Y, Matsushima K, Sato K, Tsuchiya M, Yamada Y;	
PI	Yamazaki T;	

```
XX DR WPI; 1996-105864/11.
XX
XX PT Reconstituted human antibody recognising human interleukin-8
XX PT containing mouse anti-IL8 antibody variable region sequences, has
XX PT low antigenicity in humans
XX
XX Example 4; Page 73; 125pp; Japanese.
XX
CC The present sequence is a PCR primer for pUC-WS4-VL, which encodes
CC the variable light chain from a WS4 hybridoma monoclonal antibody
CC (Mab). The hybridoma was constructed by fusing BALB/c mouse spleen
CC cells, immunised with human IL-8, with mouse myeloma P3X63-Ag8.653
CC cells. Complementarity determining region (CDR) DNA from pUC-WS4-VL
CC and its heavy chain equivalent pUC-WS4-VH, was used together with
CC human framework region DNA to construct chimaeric H and L region, V
CC region DNA. The DNA was then inserted into a HEF vector along with
CC human C-kappa and C-gamma-1, C region DNA to produce a vector
CC capable of expressing a human/murine chimaeric Mab. The Mab can be
CC used for the treatment of inflammatory diseases mediated by IL-8,
CC and as the major part of the Mab comes from a human Ab, and only
CC the CDR regions are of murine origin, the Mab has the advantage of
CC having low antigenicity to the human body when used
CC therapeutically.
CC
XX Sequence 34 BP; 9 A; 10 C; 7 G; 8 T; 0 other;
XX
XX
XX Query Match 53.3%; Score 19.2; DB 17; Length 34;
XX Best Local Similarity 75.0%; Pred. No. 1e+02;
XX Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
Oy 4 aaagctccaccatgacgcagacccaagt 35
Db 3 aaagctccaccatgacgcagctcactcagt 34
XX
XX
XX RESULT 3
XX AAT09869
XX ID AAT09869 standard; cDNA; 38 BP.
XX
XX AC AAT09869;
XX
XX DT 15-OCT-1996 (first entry)
XX
XX DE Human neurotransmitter transporter protein 5' DNA primer.
XX
XX KW Neurotransmitter transporter protein; pain therapy; stroke therapy;
XX KW amyotrophic lateral sclerosis; oligonucleotide; DNA primer; PCR;
XX KW polymerase chain reaction; ss.
XX
XX OS Synthetic.
XX
XX PN W09531539-A1.
XX
XX PD 23-NOV-1995.
XX
XX PE 16-MAY-1994; 94WO-US05363.
XX
XX PR 16-MAY-1994; 94WO-US05363.
XX PR 26-MAY-1994; 94ZA-0003696.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Fleischmann RD, Li Y;
XX
XX DR WPI; 1996-010925/01.
XX
XX PT DNA encoding neuro:transmitter transporter protein and related
XX PT (ant)agonists - useful to treat e.g., amyotrophic lateral sclerosis,
XX PT pain and stroke.
XX
XX Disclosure: Page 32; 53pp; English.
```

```
XX CC This 5' primer is used in the construction of a plasmid for
XX CC expression of recombinant NRT in COS cells. This primer contains
XX CC a BglII site followed by 21 nucleotide of NRT coding sequence
XX CC starting from the initiation codon.
XX
XX Sequence 38 BP; 14 A; 10 C; 9 G; 5 T; 0 other;
XX
XX
XX Query Match 51.7%; Score 18.6; DB 17; Length 38;
XX Best Local Similarity 72.7%; Pred. No. 1.9e+02;
XX Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
Oy 4 aaagctccaccatgacgcagacccaagt 36
Db 6 agatctgcaccatgacgcagacccaagt 38
XX
XX
XX RESULT 4
XX AAQ47027
XX ID AAQ47027 standard; DNA; 55 BP.
XX
XX AC AAQ47027;
XX
XX DT 31-JAN-1994 (first entry)
XX
XX DE HCV core sequence isolation primer #4.
XX
XX KW Precore; core; coding region; hepatitis B; virus; HBV; plasmid; PCR;
XX KW PCR; isolation; HCV; NANBH; non-A, non-B hepatitis; primers; mutation;
XX KW cytotoxic T-lymphocyte; CTL; PCR; HXHCVcore; hepatitis C; infection;
XX KW hepatocellular carcinomas; class-I; ss.
XX
XX OS Synthetic.
XX
XX PN W09315207-A.
XX
XX PD 05-AUG-1993.
XX
XX PE 04-FEB-1993; 93WO-US01009.
XX
XX PR 04-FEB-1992; 92US-0830417.
XX
XX PA (VIAG-) VIAGENE INC.
XX
XX PI Chang SMW, Jolly DJ, Lee WT, O'Dea J, Townsend K;
XX
XX DR WPI; 1993-258682/32.
XX
XX PT Treatment of hepatitis B and C, and associated carcinoma(s) -
XX PT using a vector construct directing the expression of part of
XX PT hepatitis B or C antigen
XX
XX Example 2C; Page 29; 110pp; English.
XX
XX The sequences given in AAQ47024-29 are primers which were used in the
XX isolation of the core coding region of hepatitis C virus (HCV). The
XX viral DNA which was used as a template in the PCR reaction, was
XX isolated from serum obtained from a patient with chronic non-A,
XX non-B hepatitis (NANBH). Three separate PCR reactions were performed
XX in the production of a 570 bp amplification product. This oligomer
XX was ligated into the pCRII vector and designated PCR1H-XHCVcore.
XX The isolated HCV core region may be used in a method to induce potent
XX class-I restricted protective and therapeutic cytotoxic T-lymphocyte
XX (CTL) response, and a humoral response for the treatment of hepatitis
XX B and C infections, as well as hepatocellular carcinomas.
XX
XX Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;
XX
XX
XX Query Match 51.7%; Score 18.6; DB 14; Length 55;
XX Best Local Similarity 72.7%; Pred. No. 2e+02;
XX Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

Oy 1 gcgaaagctccacatgagcagacaccaa 33  
 || |||||  
 Db 3 gcttaagcttcacacatgagcagacaccaa 35

RESULT 5  
 AAV30020  
 ID AAV30020 standard; DNA; 55 BP.  
 AC AAV30020;  
 XX  
 DT 13-AUG-1998 (first entry)  
 XX

PCR primer used to amplify a Hepatitis C virus core sequence.  
 DE  
 XX  
 KW HCV core sequence; treatment; intracellular infection; mammal;  
 KW immunogenic portion; antigen; intracellular pathogen;  
 KW bacterial infection; legionella; tuberculosis; chlamydia;  
 KW parasitic infection; rickettsia; leishmaniasis; malaria; viral infection;  
 KW Herpes; HIV; FIV; PCR primer; ss.  
 XX

OS Synthetic.  
 OS Hepatitis C virus.  
 XX  
 XX WO9812332-A1.  
 PD 26-MAR-1998.  
 XX  
 XX 16-SEP-1997; 97WO-US16453.  
 PF  
 XX 17-SEP-1996; 96US-0025267.  
 PR

PA (CHIR ) CHIRON CORP.  
 PA (SCRT ) SCRIPPS RES. INST.  
 XX

PI Lee WTL, Milich DR, Salberg M;  
 XX  
 XX WPI: 1998-217270/19.  
 DR

PT Vector construct directing expression of intracellular pathogenic  
 PT antigen - useful for, e.g. treatment of intracellular diseases in  
 PT animals such as tuberculosis and chlamydia  
 XX

XX Example 2; Page 35; 141pp; English.  
 XX

PCR primers AAV30020-21 were used to amplify a Hepatitis C virus (HCV)  
 CC core sequence, using as a template the amplification product of  
 CC primers AAV30016-17. Two consecutive stop codons are added in frame with  
 CC the HCV gene. The amplified product is cloned and used to exemplify  
 CC the invention, which describes a method for treating intracellular  
 CC infections of warm-blooded mammals. This comprises administering to the  
 CC mammal a vector construct which directs the expression of at least one  
 CC immunogenic portion of an antigen derived from an intracellular pathogen  
 CC (e.g. HBV), and also administering a protein which comprises the  
 CC immunogenic portion of the antigen. The composition is used to treat  
 CC intracellular infections within warm-blooded animals e.g. bacterial  
 CC infections such as legionella, tuberculosis and chlamydia, parasitic  
 CC infections such as rickettsia, leishmaniasis or malaria and viral  
 CC infections like Hepatitis, Herpes, HIV and FIV.  
 XX  
 XX Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;

Query Match 51.7%; Score 18.6; DB 19; Length 55;  
 Best Local Similarity 72.7%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 gcgaaagctccacatgagcagacaccaa 33  
 || |||||  
 Db 3 gcttaagcttcacacatgagcagacaccaa 35

RESULT 6  
 AAD21201  
 ID AAD21201 standard; DNA; 55 BP.  
 XX  
 AC AAD21201;  
 XX  
 DT 15-JAN-2002 (first entry)  
 XX

Sense PCR primer #8 used in the isolation of HCV core sequence.  
 DE  
 XX  
 KW Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma;  
 KW HCC; gene therapy; virucide; hepatotropic; anti-inflammatory; cytostatic;  
 KW site-directed mutagenesis; PCR primer; ss.  
 XX

OS Hepatitis C virus.  
 XX  
 PN US6297048-B1.  
 XX  
 PD 02-OCT-2001.  
 XX  
 XX 07-JUN-1995; 95US-0483511.  
 PF

PR 04-FEB-1992; 92US-0830417.  
 PR 17-MAR-1993; 93US-0032385.  
 PR 04-AUG-1993; 93US-0102132.  
 PR 05-AUG-1994; 94US-0286829.  
 PR 19-JAN-1995; 95US-0374414.  
 XX

PA (CHIR ) CHIRON CORP.  
 XX  
 XX Jolly DJ, Chang SMW, Lee WTL, Townsend K, O'Dea J;  
 PI  
 XX WPI: 2001-647290/74.  
 DR

PT New vectors that direct the (co-)expression of one or more immunogenic  
 PT portions of the hepatitis B or C virus antigen(s), useful in gene  
 PT therapy, e.g. for treating or preventing hepatitis B or C infections,  
 PT or hepatocellular carcinomas  
 XX  
 XX Example 2; Column 23; 64pp; English.  
 PS

The present invention relates to a method for treating hepatitis B or C  
 CC infections. The method involves administering a vector construct that  
 CC directs the expression of at least one immunogenic portion of hepatitis  
 CC B virus (HBV) antigen, containing HBeAg, HbCag, HbSag, S, Pre-S1, Pre-S2,  
 CC open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of  
 CC at least one immunogenic portion of a HBV antigen and at least one  
 CC immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are  
 CC useful in gene therapy, particularly for treating or preventing  
 CC hepatitis B and hepatitis C infections, as well as hepatocellular  
 CC carcinomas (HCC). The present sequence is a PCR primer used in the  
 CC isolation of HCV core sequence.  
 XX

SO Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;

Query Match 51.7%; Score 18.6; DB 22; Length 55;  
 Best Local Similarity 72.7%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 gcgaaagcttcacacatgagcagacaccaa 33  
 || |||||  
 Db 3 gcttaagcttcacacatgagcagacaccaa 35

RESULT 7  
 AAI15233  
 ID AAI15233 standard; DNA; 75 BP.  
 XX  
 AC AAI15233;  
 XX

DT 04-SEP-2000 (first entry)  
 XX





XX	PA	(HYBR-) HYBRIDON INC.
XX	P1	211man M:
XX	XX	
DR	XX	WPI; 1998-008873/01.
PT	PT	New ribozyme variants having a shortened stem-loop II region - have
PT	PT	improved catalytic activity under low magnesium conditions and low
XX	XX	turnover conditions
PS	PS	Disclosure; Page 51; 112pp; English.
XX	XX	
CC	CC	This is the nucleotide sequence of the PCR primer used for
CC	CC	amplification in the method of the invention which involves the
CC	CC	creation of ribozyme variants that have improved catalytic activity
CC	CC	under low magnesium condition. The ribozyme variant can be used to
CC	CC	cleave target RNA to control the expression of the RNA. They can be
CC	CC	used for treating diseases such as bacterial or viral infection, e.g.
CC	CC	HIV infection. They can also be used as RNA-specific restriction
CC	CC	endonucleases in the preparation of recombinant RNA molecules.
XX	XX	
SQ	SQ	Sequence 53 BP; 5 A; 13 C; 17 G; 18 T; 0 other;
XX	XX	
Query Match		50.0%; Score 18; DB 19; Length 53;
Best Local Similarity		80.8%; Pred. No. 3.6e+02;
Matches	21; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
OY	8	cttcgcacatgagccagcagcaccacaa 33
Db	52	CCTGCACCATGAGCAGCAGACCCCAAA 27
XX	XX	
RESULT 12		
AAQ44724/C		
ID	AAQ44724	standard: DNA; 82 BP.
XX	XX	
AC	AAQ44724;	
XX	XX	
DT	18-OCT-1994	(first entry)
XX	XX	
DE	Oligonucleotide used to construct humanised antibody gene cassette.	
XX	XX	
KW	Antibody; heavy chain; light chain; variable region; therapy;	
KW	Constant region; prophylaxis; prevention; allergy; identification;	
KW	allergic reaction; immunoglobulin; IGE; determination; ss.	
XX	XX	
OS	Synthetic.	
XX	XX	
PN	EP589840-A.	
XX	XX	
PD	30-MAR-1994.	
XX	XX	
PE	15-SEP-1993;	93EP-0810653.
XX	XX	
PR	24-SEP-1992;	92GB-0020228.
PR	25-SEP-1992;	92US-0952802.
XX	XX	
PA	(CTBA ) CTBA GELVY AG.	
PA	(TANO-) TANOX BIOSYSTEMS INC.	
XX	XX	
PI	Hardman N, Kolbinger F, Saldanha J;	
XX	XX	
DR	WPI; 1994-103410/13.	
XX	XX	
PT	New reshaped human monoclonal antibody specific for IGE - used	
PT	for prophylaxis or treatment of allergic reactions or qualitative	
PT	or quantitative determ. of IGE	
XX	XX	
PS	Example 3; Page 51; 68pp; English.	
XX	XX	
CC	Reshaped human monoclonal antibodies can be used in the prophylaxis	

CC	and/or treatment of allergic reactions in humans	The monoclonal
CC	antibodies can also be used for the qualitative or quantitative	determination of IgE and for the determination of surface IgE
CC	determination of IgE and for the determination of surface IgE	effective B cells. They can provide a long lasting therapeutic
CC	effective B cells. They can provide a long lasting therapeutic	effect without inducing immunogenicity as foreign proteins. Six
CC	synthetic oligonucleotides (AA044719-24) were used to construct a	humanised antibody light chain variable region gene cassette.
CC	humanised antibody light chain variable region gene cassette.	
XX		
SO	Sequence 82 BP; 11 A; 23 C; 23 G; 25 T; 0 other;	
QY	Query Match	50.0%; Score 18; DB 15; Length 82;
	Best Local Similarity	80.8%; Pred. No. 3.9e+02;
	Matches 21; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
Db	11 ccacatgagccagacacccaagt 36                         60 CCACCTTGGCGCAGGCAACAGGTG 35	
RESULT 13		
AAZ28558/C		
ID	AAZ28558 standard; DNA; 82 BP.	
XX		
AC	AAZ28558;	
XX		
DT	24-DEC-1999 (first entry)	
DE	Oligonucleotide C21-LF for creating reshaped human antibody.	
XX		
DI	Diagnosis: IGE; Immunoglobulin; body fluid; human; monoclonal antibody;	
KW	binding affinity; mouse; CDR; complementarity determining region;	
KW	allergy; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	US5958708-A.	
PD	28-SEP-1999.	
XX		
PE	07-JUN-1995; 95US-0476176.	
XX		
PR	27-SEP-1993; 93US-0127721.	
PR	25-SEP-1992; 92US-0952802.	
XX		
PA	(NOVS ) NOVARTIS CORP.	
PA	(TANO-) TANOX BIOSYSTEMS INC.	
XX		
PI	Saldanha J, Kolbinger F, Hardman N;	
XX		
DR	WPI; 1999-570765/48.	
XX		
PPT	new method for determining IGE levels in a sample	-
PS	Example 3; Column 55-56; 19pp; English.	
XX		
CC	The invention relates to a method of determining IGE levels in a body	fluid sample, by contacting the sample with a reshaped human monoclonal
CC	antibody (RA) having a binding affinity about equal to that of the	mutine CDR-donor antibody TES-C21 produced by the cell line 11133.
CC	The antibodies are useful in the diagnosis, prophylaxis and treatment	of allergy. Oligonucleotides AAZ28553-428564 are used to generate the
CC	reshaped human antibodies AAZ28546-228552.	
XX		
SO	Sequence 82 BP; 11 A; 23 C; 23 G; 25 T; 0 other;	
QY	Query Match	50.0%; Score 18; DB 20; Length 82;
	Best Local Similarity	80.8%; Pred. No. 3.9e+02;
	Matches 21; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
11	ccacatgagccagacacccaagt 36	

```

Db          60 CCACCTTGCGCCAGGACCAAGGTG 35
              ||||| | ||||| ||||| |||
RESULT 14
AI130004/C
ID AI130004 standard; DNA; 31 BP.
XX
XX AI130004;
XX
XX 18-OCT-2001 (first entry)
XX
XX Human single nucleotide polymorphism (SNP) CPT2 4.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
XX single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replace(16,C)
XX FT /tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX MO20016800-A2.
XX
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
XX
XX 07-MAR-2000; 2000US-0187510.
XX PR 22-MAY-2000; 2000US-0206129.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI: 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
XX sites, useful in methods for predicting the presence, absence or
XX severity of a particular phenotype or disorder (e.g. diabetes)
XX associated with a particular genotype -
XX
XX Claim 1; Page 62; 145pp; English.
XX
XX The invention relates to the identification of nucleic acid molecules
XX (AI129513-AI13134) from the human genome which include polymorphic sites
XX which can predispose individuals to disease. Various genes from a number
XX of individuals were resequenced and single nucleotide polymorphisms
XX (SNPs) in these genes discovered. The method is useful for predicting the
XX presence, absence or severity of a particular phenotype or disorder (e.g.
XX diabetes) associated with a particular nucleotide. The nucleic acids
XX containing the polymorphic sites may be useful in forensics and paternity
XX testing.
XX
XX Sequence 31 BP; 7 A; 4 C; 7 G; 13 T; 0 other;
XX
Query Match 48.9%; Score 17.6; DB 22; Length 31;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
QY 11 ccacatgagccaggaaccaag 34
   ||| | ||| ||||| |||||
DB 31 CCATCTGTATCCAGACATCAAG 8
RESULT 15
ABA95305
ID ABA95305 standard; DNA; 36 BP.
XX
XX ABA95305;

```

XX	04-MAR-2002	(first entry)
DT		
XX		
DE	Human tyrosyl protein sulphotransferase, TPST-2, forward PCR primer.	
XX		
XX	Human TPST-2; PCR primer: autism, tyrosyl protein sulphotransferase;	
KW	digestive enzyme; food allergy; attention deficit disorder;	
KW	obsessive compulsive disorder; Crohn's disease; Coeliac disease;	
KW	dyspraxia; eating disorder; irritable bowel syndrome; schizophrenia;	
KM	schizoaffective disorder; ulcerative colitis; chronic fatigue syndrome;	
KW	Angelman's syndrome; rheumatic fever; Sydenham's chorea;	
KM	Tourette's syndrome; Prader Willi syndrome; tics; ss.	
XX		
OS	Homo sapiens.	
PN	WO20017681-A1.	
XX		
PD	18-OCT-2001.	
XX		
XX	05-APR-2001; 2001WO-GB01569.	
FE		
XX	06-APR-2000; 2000GB-0008326.	
PR	(SHSI-) SHS INT LTD.	
XX		
PA		
PI	Maring R, Phoenix J;	
XX		
DR	WPI: 2002-010948/01.	
PT	Detecting predisposition to autism and related diseases by detecting	
PT	reduced tyrosyl protein sulfotransferase (TPST) activity and treating	
PT	those diseases by enhancing TPST or cholestyramine activity	-
XX		
PS	Disclosure; Page 9; 42pp; English.	
XX		
CC	The present invention relates to a method for detecting predisposition to	
CC	autism and related diseases. The method comprises assaying a sample in	
CC	vitro for reduced tyrosyl protein sulphotransferase (TPST) level compared	
CC	to a reference sample. TPST catalyses the transfer of sulphate from	
CC	3-phosphoadenosine 5'-phosphosulphate (PAPS) to tyrosine residues within	
CC	highly acidic regions of polypeptides. Autism-related diseases include	
CC	those associated with a 'leaky' gastrointestinal tract or inadequate	
CC	digestive enzymes leading to increased opiod activity, including gluten	
CC	or casein intolerance or food allergy, attention deficit disorder,	
CC	obsessive compulsive disorder, Crohn's disease, Coeliac disease,	
CC	particularly gluten-sensitive ataxias, dyspraxia, eating disorders such	
CC	as anorexia, irritable bowel syndrome, schizophrenia, schizoaffective	
CC	disorder and ulcerative colitis. Also related are those associated with	
CC	chronic CCK activity, including attention deficit hyperactivity disorder,	
CC	chronic fatigue syndrome and diseases commonly treated with dopamine	
CC	antagonists. Other diseases related to autism are those implicated as	
CC	genetically linked, including Angelman's syndrome, rheumatic fever,	
CC	Sydenham's chorea, Tourette's syndrome, Prader Willi syndrome and the	
CC	development of tics and diseases involving language problems. The present	
CC	sequence is a PCR primer, which can be used to amplify the entire open	
CC	reading frame (ORF) of human TPST-2 cDNA.	
XX		
XX		
Sequence	36 BP; 6 A; 9 C; 15 G; 6 T; 0 other;	
Query Match	48.9%; Score 17.6; DB 24; Length 36;	
Best Local Similarity	83.3%; Pred. No. 4, Be+02;	
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
1	ggcgaagcttcacacatgagccag 24	
I		
db	1 ggcgaagcttcacacatgagccag 24	

Search completed: June 22, 2002, 05:39:59  
Job time: 5074 sec





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## OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:14:30 ; Search time 98.05 Seconds  
(Without alignments)  
90.187 Million cell updates/sec

Title: US-09-927-267-12

Perfect score: 36

Sequence: 1 gcgaagctccaccatgagccagacacaaagt 36

## Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 613726

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

## Database :

1: Issued\_Patents\_MA:\*  
2: /cgn2\_6/ptodata/2/1na/5A\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/6B\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.2	53.3	34	2	US-08-765-783A-30
2	19.2	53.3	34	3	US-08-921-100-30
3	19.2	53.3	34	3	US-08-880-142-30
4	19.2	53.3	34	3	US-08-902-201-30
5	19.2	53.3	34	4	US-09-416-557-30
6	18.6	51.7	38	1	US-08-424-424B-5
7	18.6	51.7	55	4	US-08-483-511-14
8	18.6	51.7	55	5	PCT-US93-01009-14
9	18	50.0	82	2	US-08-476-176B-24
10	18	50.0	82	3	US-08-127-721A-24
11	17	47.2	82	3	US-08-485-246A-24
12	17	47.2	43	1	US-07-969-931-25
13	17	47.2	43	1	US-07-855-417A-25
14	17	47.2	96	1	US-08-479-783A-57
15	17	47.2	96	1	US-08-479-725-57
16	17	47.2	96	1	US-08-618-693-57
17	17	47.2	96	4	US-08-973-124-146
18	17	47.2	96	4	US-08-991-743C-57
19	17	47.2	96	5	PCT-US96-08014-146
20	16.8	46.7	31	5	PCT-US94-07091-1
21	16.8	46.7	35	4	US-08-848-760B-6
22	16.8	46.7	45	2	US-08-588-201-9
23	16.8	46.7	45	2	US-09-169-605-9
24	16.8	46.7	45	3	US-08-893-327-9
25	16.4	45.6	35	1	US-08-137-117D-40
26	16.4	45.6	35	1	US-08-436-717-40
27	16.2	45.0	30	3	US-08-557-210A-25

28	16.2	45.0	36	2	US-08-811-028-24	Sequence 24, Appl
29	16.2	45.0	36	2	US-08-811-028-25	Sequence 25, Appl
30	16	44.4	29	1	US-07-946-421-33	Sequence 33, Appl
31	16	44.4	36	1	US-08-137-117D-48	Sequence 48, Appl
32	16	44.4	36	1	US-08-436-717-48	Sequence 48, Appl
33	16	44.4	37	1	US-08-462-894-33	Sequence 43, Appl
34	16	44.4	37	1	US-08-206-185-33	Sequence 37, Appl
35	15.8	43.9	36	3	US-08-767-942A-37	Sequence 37, Appl
36	15.8	43.9	56	4	US-09-052-521C-31	Sequence 31, Appl
37	15.6	43.3	38	1	US-08-208-886C-69	Sequence 69, Appl
38	15.6	43.3	38	1	US-08-704-744-69	Sequence 69, Appl
39	15.6	43.3	52	1	US-08-427-097-22	Sequence 22, Appl
40	15.6	43.3	52	2	US-08-878-957-22	Sequence 22, Appl
41	15.4	42.8	34	4	US-08-646-265A-30	Sequence 30, Appl
42	15.2	42.2	28	1	US-08-487-753-10	Sequence 10, Appl
43	15.2	42.2	28	2	US-08-480-065-10	Sequence 10, Appl
44	15.2	42.2	28	3	US-08-487-744-10	Sequence 10, Appl
45	15.2	42.2	28	5	PCT-US93-09167-10	Sequence 10, Appl
46	15.2	42.2	29	2	US-08-143-311B-22	Sequence 22, Appl
47	15.2	42.2	30	4	US-09-277-457-9	Sequence 9, Appl
48	15.2	42.2	30	4	US-09-277-457-21	Sequence 21, Appl
49	15.2	42.2	47	2	US-08-467-603-68	Sequence 98, Appl
50	15.2	42.2	47	2	US-08-466-793-98	Sequence 98, Appl
51	15.2	42.2	47	2	US-08-491-861A-98	Sequence 98, Appl
52	15	41.7	34	3	US-08-836-561-14	Sequence 12, Appl
53	15	41.7	34	3	US-08-836-561-14	Sequence 12, Appl
54	15	41.7	36	1	US-08-137-117D-46	Sequence 46, Appl
55	15	41.7	36	1	US-08-436-717-46	Sequence 46, Appl
56	15	41.7	36	1	US-08-400-115-13	Sequence 46, Appl
57	15	41.7	37	2	US-08-765-783A-31	Sequence 13, Appl
58	15	41.7	37	3	US-08-921-100-31	Sequence 31, Appl
59	15	41.7	37	3	US-08-880-142-31	Sequence 31, Appl
60	15	41.7	37	3	US-08-902-201-31	Sequence 31, Appl
61	15	41.7	37	3	US-09-416-557-31	Sequence 31, Appl
62	15	41.7	41	3	US-08-718-728-7	Sequence 7, Appl
63	15	41.7	41	4	US-09-221-844-7	Sequence 7, Appl
64	15	41.7	41	5	PCT-US95-03323A-7	Sequence 7, Appl
65	15	41.7	42	1	US-08-154-916-4	Sequence 4, Appl
66	15	41.7	43	4	US-08-646-265A-32	Sequence 32, Appl
67	15	41.7	44	1	US-08-253-877C-44	Sequence 44, Appl
68	15	41.7	44	2	US-08-452-164A-44	Sequence 44, Appl
69	15	41.7	44	2	US-08-470-139-3	Sequence 3, Appl
70	15	41.7	44	4	US-08-569-147-25	Sequence 25, Appl
71	15	41.7	44	4	US-08-976-183A-20	Sequence 20, Appl
72	15	41.7	44	4	US-09-347-061-3	Sequence 3, Appl
73	15	41.7	58	1	US-08-146-422-22	Sequence 22, Appl
74	15	41.7	58	1	US-08-146-424-23	Sequence 23, Appl
75	15	41.7	58	1	US-08-468-865-2	Sequence 2, Appl
76	15	41.7	58	1	US-08-253-575-3	Sequence 3, Appl
77	15	41.7	58	1	US-08-626-554-4	Sequence 4, Appl
78	15	41.7	58	1	US-08-693-709-5	Sequence 5, Appl
79	14.8	41.1	26	1	US-08-010-997-7	Sequence 7, Appl
80	14.8	41.1	26	1	US-08-612-551-7	Sequence 7, Appl
81	14.8	41.1	26	2	US-09-006-232-7	Sequence 7, Appl
82	14.8	41.1	26	3	US-09-211-408-7	Sequence 7, Appl
83	14.8	41.1	30	5	PCT-US93-07672-7	Sequence 7, Appl
84	14.8	41.1	43	4	US-09-042-353-398	Sequence 398, Appl
85	14.8	41.1	43	4	US-08-758-417A-248	Sequence 398, Appl
86	14.8	41.1	62	4	US-08-483-511-13	Sequence 13, Appl
87	14.8	41.1	62	5	PCT-US93-01009-13	Sequence 13, Appl
88	14.8	41.1	69	4	US-08-591-632-71	Sequence 71, Appl
89	14.6	40.6	26	2	US-08-859-998-301	Sequence 301, Appl
90	14.6	40.6	26	4	US-09-223-928-101	Sequence 301, Appl
91	14.6	40.6	27	4	US-08-584-048-3186	Sequence 3186, Appl
92	14.6	40.6	28	2	US-08-132-9900A-20	Sequence 20, Appl
93	14.6	40.6	31	4	US-08-676-645-338	Sequence 338, Appl
94	14.6	40.6	31	4	US-09-194-285-48	Sequence 48, Appl
95	14.6	40.6	39	4	US-08-849-602C-22	Sequence 22, Appl
96	14.6	40.6	60	3	US-08-911-894-59	Sequence 59, Appl
97	14.6	40.6	86	1	US-08-447-169A-159	Sequence 159, Appl
98	14.4	40.0	20	2	US-08-765-783A-70	Sequence 70, Appl
99	14.4	40.0	20	3	US-08-921-100-70	Sequence 70, Appl
100	14.4	40.0	20	3	US-08-880-142-20	Sequence 20, Appl

101	14.4	40.0	20	3	US-08-902-201-70	Sequence 70, Appl	174	14	38.9	56	1	US-08-612-551-8	Sequence 8, Appl1
102	14.4	40.0	20	4	US-09-416-557-70	Sequence 70, Appl	175	14	38.9	56	2	US-09-006-232-8	Sequence 8, Appl1
103	14.4	40.0	25	1	US-08-601-419-6	Sequence 6, Appl1	176	14	38.9	56	3	US-09-211-408-8	Sequence 8, Appl1
104	14.4	40.0	32	1	US-08-137-117D-73	Sequence 73, Appl	177	14	38.9	81	1	US-08-447-169A-192	Sequence 192, App
105	14.4	40.0	32	1	US-08-436-717-73	Sequence 73, Appl	178	14	38.9	98	1	US-08-447-172A-38	Sequence 38, Appl
106	14.4	40.0	32	4	US-09-109-879-83	Sequence 83, Appl	179	13.8	38.3	27	4	US-08-584-040-611	Sequence 611, App
107	14.4	40.0	32	4	US-09-522-666-12	Sequence 12, Appl	180	13.8	38.3	27	4	US-08-584-040-3614	Sequence 3614, Ap
108	14.4	40.0	33	1	US-08-086-439C-4	Sequence 4, Appl1	181	13.8	38.3	27	4	US-08-584-040-5029	Sequence 5029, Ap
109	14.4	40.0	33	1	US-08-434-877-4	Sequence 4, Appl1	182	13.8	38.3	27	4	US-08-584-040-6754	Sequence 6754, Ap
110	14.4	40.0	34	4	US-09-006-353A-23	Sequence 23, Appl	183	13.8	38.3	34	4	US-08-221-767-15	Sequence 15, Appl
111	14.4	40.0	34	4	US-08-043-646-6	Sequence 6, Appl1	184	13.8	38.3	35	1	US-07-941-414-6	Sequence 6, Appl1
112	14.4	40.0	36	1	US-08-137-117D-41	Sequence 41, Appl	185	13.8	38.3	36	1	US-08-249-377A-6	Sequence 6, Appl1
113	14.4	40.0	36	1	US-08-436-717-41	Sequence 41, Appl	186	13.8	38.3	36	2	US-08-816-735-5	Sequence 5, Appl1
114	14.4	40.0	41	4	US-09-564-805-102	Sequence 102, App	187	13.8	38.3	36	2	US-08-749-337-6	Sequence 6, Appl1
115	14.4	40.0	45	1	US-08-208-886C-30	Sequence 30, Appl	188	13.8	38.3	36	4	US-09-090-673-5	Sequence 5, Appl1
116	14.4	40.0	45	1	US-08-704-744-30	Sequence 30, Appl	189	13.8	38.3	45	1	US-08-220-606B-11	Sequence 11, Appl
117	14.4	40.0	45	1	US-08-469-557-30	Sequence 30, Appl	190	13.8	38.3	45	1	US-08-171-389-388	Sequence 388, App
118	14.4	40.0	45	2	US-08-290-793B-30	Sequence 30, Appl	191	13.8	38.3	50	1	US-08-123-936-388	Sequence 388, App
119	14.4	40.0	55	2	US-08-373-190-49	Sequence 49, Appl	192	13.8	38.3	50	2	US-08-475-228A-388	Sequence 388, App
120	14.4	40.0	55	3	US-08-438-190A-49	Sequence 49, Appl	193	13.8	38.3	50	3	US-08-482-080A-388	Sequence 388, App
121	14.4	40.0	55	3	US-09-287-145A-49	Sequence 49, Appl	194	13.8	38.3	50	5	PCT-US93-12388-388	Sequence 388, App
122	14.4	40.0	55	4	US-09-556-111-49	Sequence 49, Appl	195	13.8	38.3	54	6	5240845-40	Patent No. 5240845
123	14.4	40.0	60	1	US-08-219-012-58	Sequence 58, Appl	196	13.8	38.3	55	5	PCT-US92-10024-5	Sequence 5, Appl1
124	14.4	40.0	60	4	US-08-687-421-246	Sequence 246, App	197	13.8	38.3	55	5	PCT-US92-10024-6	Sequence 6, Appl1
125	14.4	40.0	74	1	US-08-208-886C-24	Sequence 24, Appl	198	13.8	38.3	55	6	5240845-31	Patent No. 5240845
126	14.4	40.0	74	1	US-08-704-744-24	Sequence 24, Appl	199	13.8	38.3	60	2	US-08-657-884-1	Sequence 1, Appl1
127	14.4	40.0	74	1	US-08-469-557-24	Sequence 24, Appl	200	13.8	38.3	60	2	US-08-657-884-3	Sequence 3, Appl1
128	14.4	40.0	74	2	US-08-290-793B-24	Sequence 24, Appl	201	13.8	38.3	60	3	US-08-911-894-60	Sequence 60, Appl
129	14.4	40.0	98	4	US-09-153-586-19	Sequence 19, Appl	202	13.8	38.3	60	4	US-09-158-980-1	Sequence 1, Appl1
130	14.4	40.0	98	4	US-09-153-586-20	Sequence 20, Appl	203	13.8	38.3	60	4	US-09-158-980-3	Sequence 3, Appl1
131	14.4	39.4	27	3	US-08-985-162-128	Sequence 128, Ap	204	13.8	38.3	80	1	US-08-208-886C-21	Sequence 21, Appl
132	14.2	39.4	27	4	US-08-591-632-72	Sequence 72, Appl	205	13.8	38.3	80	1	US-08-704-744-21	Sequence 21, Appl
133	14.2	39.4	30	4	US-09-374-135-19	Sequence 19, Appl	206	13.8	38.3	80	1	US-08-469-557-21	Sequence 21, Appl
134	14.2	39.4	33	1	US-07-915-720D-10	Sequence 10, Appl	207	13.8	38.3	80	2	US-08-290-793B-21	Sequence 21, Appl
135	14.2	39.4	33	1	US-07-915-720D-11	Sequence 11, Appl	208	13.8	38.3	86	4	US-08-464-700-21	Sequence 21, Appl
136	14.2	39.4	33	3	US-09-025-543-11	Sequence 11, Appl	209	13.6	37.8	96	4	US-08-464-700-46	Sequence 46, Appl
137	14.2	39.4	33	3	US-09-025-543-11	Sequence 11, Appl	210	13.6	37.8	20	4	US-09-487-368A-178	Sequence 178, App
138	14.2	39.4	40	3	US-08-718-738-11	Sequence 11, Appl	211	13.6	37.8	25	2	US-08-794-494-13	Sequence 13, Appl
139	14.2	39.4	40	3	US-09-221-844-11	Sequence 11, Appl	212	13.6	37.8	27	3	US-08-985-162-1123	Sequence 1123, Ap
140	14.2	39.4	40	5	PCT-US95-03323A-11	Sequence 11, Appl	213	13.6	37.8	31	4	US-08-679-645-313	Sequence 313, App
141	14.2	39.4	54	5	PCT-US92-01303-13	Sequence 13, Appl	214	13.6	37.8	31	4	US-08-679-645-383	Sequence 383, App
142	14	38.9	25	4	US-08-646-265A-96	Sequence 96, Appl	215	13.6	37.8	31	4	US-08-679-645-423	Sequence 423, App
143	14	38.9	27	4	US-08-584-040-45	Sequence 45, Appl	216	13.6	37.8	32	2	US-08-640-808-3	Sequence 3, Appl1
144	14	38.9	27	4	US-08-584-040-3477	Sequence 3477, Ap	217	13.6	37.8	36	1	US-08-021-623C-16	Sequence 16, Appl
145	14	38.9	27	4	US-08-584-040-6977	Sequence 6977, Ap	218	13.6	37.8	36	1	US-07-946-421-41	Sequence 41, Appl
146	14	38.9	27	4	US-08-584-040-7208	Sequence 7208, Ap	219	13.6	37.8	36	4	US-08-748-541-12	Sequence 12, Appl
147	14	38.9	33	1	US-08-438-639-25	Sequence 25, Appl	220	13.6	37.8	38	4	US-09-564-805-104	Sequence 104, App
148	14	38.9	33	1	US-07-813-338A-25	Sequence 25, Appl	221	13.6	37.8	45	1	US-08-331-398A-30	Sequence 30, Appl
149	14	38.9	33	2	US-08-577-492-23	Sequence 23, Appl	222	13.6	37.8	45	2	US-08-331-397B-30	Sequence 30, Appl
150	14	38.9	33	3	US-08-441-971-100	Sequence 100, App	223	13.6	37.8	45	2	US-08-759-804A-30	Sequence 30, Appl
151	14	38.9	33	3	US-08-221-653-100	Sequence 100, App	224	13.6	37.8	45	4	US-09-227-693-30	Sequence 30, Appl
152	14	38.9	33	4	US-08-442-144A-100	Sequence 100, App	225	13.6	37.8	48	4	US-09-485-737B-36	Sequence 36, Appl
153	14	38.9	33	4	US-09-079-630-23	Sequence 23, Appl	226	13.6	37.8	69	4	US-08-729-601A-38	Sequence 38, Appl
154	14	38.9	33	4	US-08-441-970-100	Sequence 100, App	227	13.6	37.8	80	1	US-08-447-169A-187	Sequence 187, App
155	14	38.9	33	4	US-09-051-696-12	Sequence 12, Appl	228	13.6	37.8	80	2	US-08-548-974-16	Sequence 16, Appl
156	14	38.9	34	3	US-08-434-099A-8	Sequence 8, Appl1	229	13.6	37.8	81	2	US-08-548-974-14	Sequence 14, Appl
157	14	38.9	37	2	US-08-400-115-14	Sequence 14, Appl	230	13.6	37.8	81	2	US-08-548-974-18	Sequence 18, Appl
158	14	38.9	37	2	US-08-765-783A-38	Sequence 38, Appl	231	13.4	37.2	24	1	US-07-923-724-12	Sequence 12, Appl
159	14	38.9	37	3	US-08-921-100-38	Sequence 38, Appl	232	13.4	37.2	24	2	US-08-609-426A-12	Sequence 12, Appl
160	14	38.9	37	3	US-08-880-142-38	Sequence 38, Appl	233	13.4	37.2	27	3	US-08-513-974B-94	Sequence 94, Appl
161	14	38.9	37	3	US-08-902-201-38	Sequence 38, Appl	234	13.4	37.2	27	4	US-08-584-040-486	Sequence 486, App
162	14	38.9	37	4	US-09-416-557-38	Sequence 38, Appl	235	13.4	37.2	27	4	US-08-584-040-665	Sequence 665, Ap
163	14	38.9	38	1	US-08-808-303-10	Sequence 10, Appl	236	13.4	37.2	31	3	US-08-823-110-15	Sequence 15, Appl
164	14	38.9	38	4	US-08-996-533-10	Sequence 10, Appl	237	13.4	37.2	31	3	US-08-604-299-15	Sequence 5, Appl1
165	14	38.9	40	1	US-08-447-169A-227	Sequence 227, App	238	13.4	37.2	37	2	US-08-431-117A-7	Sequence 7, Appl1
166	14	38.9	42	1	US-08-683-877-6	Sequence 6, Appl1	239	13.4	37.2	37	2	US-08-761-277A-66	Sequence 66, Appl
167	14	38.9	54	1	US-08-146-422-21	Sequence 21, Appl	240	13.4	37.2	41	2	US-08-918-146-69	Sequence 69, Appl
168	14	38.9	54	1	US-08-146-424-22	Sequence 22, Appl	241	13.4	37.2	42	4	US-08-693-291-2	Sequence 2, Appl1
169	14	38.9	54	1	US-08-469-856-1	Sequence 1, Appl1	242	13.4	37.2	58	1	US-08-348-578-39	Sequence 39, Appl
170	14	38.9	54	1	US-08-253-575-2	Sequence 2, Appl1	243	13.4	37.2	60	4	US-09-348-578-39	Sequence 1, Appl
171	14	38.9	54	1	US-08-626-554-3	Sequence 3, Appl1	244	13.4	37.2	69	2	PCT-US91-02942-13	Sequence 13, Appl
172	14	38.9	54	1	US-08-693-709-4	Sequence 4, Appl1	245	13.4	37.2	69	5	PCT-US93-08327-1	Sequence 1, Appl1
173	14	38.9	56	1	US-08-010-997-8	Sequence 8, Appl1	246	13.4	37.2	69	5		

C 247	13.4	37.2	71	4	US-09-025-769B-150	Sequence 150, App	320	13.2	36.7	60	2	US-08-053-451B-162	Sequence 162, App
C 248	13.4	37.2	81	1	US-08-253-877C-24	Sequence 24, Appl	321	13.2	36.7	60	4	US-09-158-980-5	Sequence 4, Appl1
C 249	13.4	37.2	81	2	US-08-452-164A-24	Sequence 24, Appl	322	13.2	36.7	60	4	US-09-158-980-5	Sequence 5, Appl1
C 250	13.4	37.2	81	3	US-08-603-024-23	Sequence 22, Appl	323	13.2	36.7	62	4	US-08-483-511-15	Sequence 15, Appl1
C 251	13.4	37.2	81	4	US-08-976-183A-42	Sequence 42, Appl	324	13.2	36.7	62	5	PCT-US93-01009-15	Sequence 15, Appl
C 252	13.4	37.2	89	4	US-09-153-586-7	Sequence 7, Appl1	325	13.2	36.7	64	1	US-08-429-181-32	Sequence 32, Appl
C 253	13.2	36.7	20	3	US-09-377-310-17	Sequence 17, Appl	326	13.2	36.7	64	1	US-08-164-388-32	Sequence 32, Appl
C 254	13.2	36.7	20	3	US-09-484-345-15	Sequence 15, Appl	327	13.2	36.7	67	1	US-07-931-473B-314	Sequence 314, Appl
C 255	13.2	36.7	20	3	US-09-484-345-16	Sequence 16, Appl	328	13.2	36.7	67	1	US-07-714-131C-314	Sequence 314, App
C 256	13.2	36.7	22	1	US-08-242-403A-29	Sequence 29, Appl	329	13.2	36.7	67	1	US-08-412-110-314	Sequence 314, App
C 257	13.2	36.7	22	1	US-08-774-128-29	Sequence 29, Appl	330	13.2	36.7	67	1	US-08-409-442A-314	Sequence 314, App
C 258	13.2	36.7	22	5	PCT-US95-05602-29	Sequence 29, Appl	331	13.2	36.7	67	2	US-08-469-609A-314	Sequence 314, App
C 259	13.2	36.7	22	5	PCT-US95-05816-29	Sequence 29, Appl	332	13.2	36.7	67	3	US-09-143-190-314	Sequence 314, App
C 260	13.2	36.7	27	1	US-08-758-306-1190	Sequence 1190, Ap	333	13.2	36.7	78	2	US-08-680-326-16	Sequence 46, Appl
C 261	13.2	36.7	27	2	US-08-459-101A-5	Sequence 5, Appl1	334	13.2	36.7	78	2	US-08-680-326-17	Sequence 47, Appl
C 262	13.2	36.7	27	3	US-08-985-162-1080	Sequence 1080, Ap	335	13.2	36.7	82	4	US-09-229-212A-11	Sequence 11, Appl
C 263	13.2	36.7	27	4	US-08-584-040-518	Sequence 518, App	336	13.2	36.7	82	4	US-09-229-212A-11	Sequence 12, Appl
C 264	13.2	36.7	30	1	US-08-137-117D-93	Sequence 93, Appl	337	13.2	36.7	82	4	US-09-229-212A-12	Sequence 12, Appl
C 265	13.2	36.7	30	1	US-08-436-717-93	Sequence 93, Appl	338	13.2	36.7	84	1	US-08-480-434-43	Sequence 43, Appl
C 266	13.2	36.7	31	1	US-08-592-406-29	Sequence 29, Appl	339	13.2	36.7	84	2	US-08-053-451B-43	Sequence 43, Appl
C 267	13.2	36.7	33	3	US-08-477-460B-8	Sequence 8, Appl1	340	13.2	36.7	86	1	US-08-479-783A-34	Sequence 34, Appl
C 268	13.2	36.7	33	3	US-08-379-516-8	Sequence 8, Appl1	341	13.2	36.7	86	1	US-08-479-725-34	Sequence 34, Appl
C 269	13.2	36.7	33	4	US-09-329-916-8	Sequence 8, Appl1	342	13.2	36.7	86	1	US-08-618-693-34	Sequence 34, Appl
C 270	13.2	36.7	33	4	US-08-485-372A-8	Sequence 8, Appl1	343	13.2	36.7	86	4	US-08-973-124-123	Sequence 123, App
C 271	13.2	36.7	33	4	US-09-409-006A-8	Sequence 8, Appl1	344	13.2	36.7	86	4	US-08-991-743C-34	Sequence 34, Appl
C 272	13.2	36.7	33	5	PCT-US93-07422-8	Sequence 8, Appl1	345	13.2	36.7	86	5	PCT-US96-08014-123	Sequence 123, App
C 273	13.2	36.7	36	1	US-07-915-720D-2	Sequence 2, Appl1	346	13.2	36.7	89	1	US-07-918-953-2	Sequence 2, Appl1
C 274	13.2	36.7	36	1	US-09-025-543-2	Sequence 2, Appl1	347	13.2	36.7	89	1	US-08-081-661-2	Sequence 2, Appl1
C 275	13.2	36.7	37	1	US-08-372-556-1	Sequence 1, Appl1	348	13.2	36.7	91	1	US-08-306-618B-31	Sequence 31, Appl
C 276	13.2	36.7	37	3	US-08-892-747-1	Sequence 1, Appl1	349	13.2	36.7	91	5	PCT-US93-06551-73	Sequence 73, Appl
C 277	13.2	36.7	38	4	US-08-943-136-13	Sequence 13, Appl	350	13.2	36.7	92	1	US-08-480-434-40	Sequence 40, Appl
C 278	13.2	36.7	38	4	US-08-973-518-13	Sequence 13, Appl	351	13.2	36.7	92	2	US-08-053-451B-40	Sequence 40, Appl
C 279	13.2	36.7	40	1	US-08-761-277A-64	Sequence 64, Appl	352	13.2	36.7	97	1	US-07-918-953-1	Sequence 1, Appl1
C 280	13.2	36.7	41	1	US-07-931-473B-295	Sequence 295, App	353	13.2	36.7	97	1	US-08-081-661-1	Sequence 1, Appl1
C 281	13.2	36.7	41	1	US-07-714-131C-296	Sequence 296, App	354	13.2	36.1	15	1	US-08-305-699-1	Sequence 1, Appl1
C 282	13.2	36.7	41	1	US-08-412-110-296	Sequence 296, App	355	13.2	36.1	21	2	US-08-733-825-5	Sequence 5, Appl1
C 283	13.2	36.7	41	1	US-08-409-442A-296	Sequence 296, App	356	13.2	36.1	25	1	US-08-601-419-5	Sequence 5, Appl1
C 284	13.2	36.7	41	2	US-08-469-609A-296	Sequence 296, App	C 357	13.2	36.1	27	4	US-08-758-306-594	Sequence 594, App
C 285	13.2	36.7	41	3	US-09-143-190-296	Sequence 296, App	C 358	13.2	36.1	27	4	US-08-584-040-1634	Sequence 3542, App
C 286	13.2	36.7	44	1	US-08-106-078-7	Sequence 7, Appl1	C 359	13.2	36.1	27	4	US-08-584-040-1634	Sequence 4634, App
C 287	13.2	36.7	44	1	US-08-591-192-7	Sequence 7, Appl1	C 360	13.2	36.1	27	4	US-08-584-040-1634	Sequence 4634, App
C 288	13.2	36.7	44	1	US-08-253-877C-45	Sequence 45, Appl	C 361	13.2	36.1	28	2	US-08-859-998-1206	Sequence 1206, App
C 289	13.2	36.7	44	2	US-08-452-164A-45	Sequence 45, Appl	C 362	13.2	36.1	28	4	US-09-203-649-9	Sequence 9, Appl1
C 290	13.2	36.7	45	2	US-08-572-959-1	Sequence 1, Appl1	C 363	13.2	36.1	28	4	US-09-225-928-1206	Sequence 1206, App
C 291	13.2	36.7	45	3	US-08-817-452-1	Sequence 1, Appl1	364	13.2	36.1	31	3	US-08-726-136-19	Sequence 19, Appl
C 292	13.2	36.7	45	3	US-08-938-830-54	Sequence 54, Appl	365	13.2	36.1	31	3	US-09-103-434-19	Sequence 19, Appl
C 293	13.2	36.7	45	4	US-09-242-536-1	Sequence 1, Appl1	366	13.2	36.1	31	4	US-09-687-594-19	Sequence 19, Appl
C 294	13.2	36.7	45	4	US-09-199-737-46	Sequence 46, Appl	C 367	13.2	36.1	34	2	US-08-465-095-1	Sequence 1, Appl1
C 295	13.2	36.7	48	1	US-08-244-626-53	Sequence 33, Appl	C 368	13.2	36.1	34	2	US-08-465-095-13	Sequence 13, Appl1
C 296	13.2	36.7	48	2	US-08-039-198B-29	Sequence 29, Appl	C 369	13.2	36.1	34	5	PCT-US94-00300-1	Sequence 1, Appl1
C 297	13.2	36.7	48	2	US-08-449-645A-24	Sequence 24, Appl	C 370	13.2	36.1	34	5	PCT-US94-00300-13	Sequence 13, Appl1
C 298	13.2	36.7	48	2	US-08-702-367A-24	Sequence 24, Appl	C 371	13.2	36.1	35	3	US-08-967-272-5	Sequence 5, Appl1
C 299	13.2	36.7	48	2	US-08-182-067-34	Sequence 34, Appl	C 372	13.2	36.1	35	3	US-08-467-420A-64	Sequence 64, Appl
C 300	13.2	36.7	48	2	US-08-465-313-34	Sequence 34, Appl	C 373	13.2	36.1	36	1	US-08-470-110A-64	Sequence 64, Appl
C 301	13.2	36.7	48	3	US-09-109-063-23	Sequence 23, Appl	C 374	13.2	36.1	36	1	US-08-667-769A-64	Sequence 64, Appl
C 302	13.2	36.7	48	5	PCT-US95-04681-24	Sequence 24, Appl	C 375	13.2	36.1	36	2	US-08-940-371-64	Sequence 64, Appl
C 303	13.2	36.7	49	1	US-08-242-403A-21	Sequence 21, Appl	C 376	13.2	36.1	36	5	PCT-US95-17082A-64	Sequence 64, Appl
C 304	13.2	36.7	49	1	US-08-774-128-21	Sequence 21, Appl	377	13.2	36.1	38	1	US-08-024-253-22	Sequence 22, Appl
C 305	13.2	36.7	49	5	PCT-US95-05602-21	Sequence 21, Appl	378	13.2	36.1	39	1	US-08-466-093-331	Sequence 231, App
C 306	13.2	36.7	49	5	PCT-US95-05816-21	Sequence 21, Appl	379	13.2	36.1	39	1	US-08-444-733-231	Sequence 231, App
C 307	13.2	36.7	50	2	US-08-053-451B-137	Sequence 137, App	380	13.2	36.1	39	2	US-08-464-134-231	Sequence 231, App
C 308	13.2	36.7	50	2	US-08-053-451B-139	Sequence 139, App	381	13.2	36.1	39	2	US-08-461-361-231	Sequence 231, App
C 309	13.2	36.7	50	4	US-09-390-867A-42	Sequence 42, Appl	382	13.2	36.1	39	2	US-08-483-910-331	Sequence 231, App
C 310	13.2	36.7	50	4	US-09-548-260-42	Sequence 42, Appl	383	13.2	36.1	39	3	US-09-090-793-49	Sequence 49, Appl
C 311	13.2	36.7	58	2	US-08-484-093B-39	Sequence 39, Appl	384	13.2	36.1	39	5	PCT-US91-02942-60	Sequence 60, Appl
C 312	13.2	36.7	58	2	US-08-484-150B-39	Sequence 39, Appl	385	13.2	36.1	41	4	US-08-165-919A-9	Sequence 9, Appl1
C 313	13.2	36.7	58	2	US-08-484-596A-39	Sequence 39, Appl	386	13.2	36.1	41	5	PCT-US94-14073-9	Sequence 9, Appl1
C 314	13.2	36.7	58	2	US-08-480-150A-39	Sequence 39, Appl	387	13.2	36.1	42	2	US-08-124-981A-18	Sequence 18, Appl1
C 315	13.2	36.7	58	3	US-08-458-731-39	Sequence 39, Appl	388	13.2	36.1	42	3	US-09-037-190-16	Sequence 16, Appl
C 316	13.2	36.7	58	3	US-08-149-223A-39	Sequence 39, Appl	389	13.2	36.1	42	3	US-09-037-192-16	Sequence 16, Appl
C 317	13.2	36.7	60	2	US-08-657-884-4	Sequence 4, Appl1	390	13.2	36.1	42	3	US-09-037-143-16	Sequence 16, Appl
C 318	13.2	36.7	60	2	US-08-657-884-5	Sequence 5, Appl1	391	13.2	36.1	42	4	US-09-049-661-16	Sequence 16, Appl
C 319	13.2	36.7	60	2	US-08-379-057-4	Sequence 4, Appl1	392	13.2	36.1	42	4	US-08-260-174-16	Sequence 16, Appl

393	13	35.1	42	4	US-09-338-128A-16	Sequence 16, Appl	C 466	12.8	35.6	34	1	US-08-264-115-7	Sequence 7, Appl1
394	13	36.1	42	4	US-09-232-346-16	Sequence 16, Appl	467	12.8	35.6	36	1	US-08-391-000-40	Sequence 40, Appl
395	13	36.1	43	2	US-08-116-778E-14	Sequence 14, Appl	468	12.8	35.6	36	2	US-08-741-931-40	Sequence 40, Appl
396	13	36.1	43	2	US-08-438-562-14	Sequence 14, Appl	469	12.8	35.6	38	4	US-09-476-299-48	Sequence 48, Appl
397	13	36.1	43	2	US-08-483-528B-14	Sequence 14, Appl	470	12.8	35.6	38	4	US-09-609-154-48	Sequence 48, Appl
398	13	36.1	43	3	US-08-673-799C-14	Sequence 14, Appl	471	12.8	35.6	39	1	US-08-253-877C-47	Sequence 47, Appl
399	13	36.1	46	1	US-08-328-152A-24	Sequence 24, Appl	472	12.8	35.6	39	2	US-08-452-164A-79	Sequence 47, Appl
400	13	36.1	48	1	US-08-040-548-12	Sequence 12, Appl	C 473	12.8	35.6	39	4	US-08-026-143B-29	Sequence 29, Appl
401	13	36.1	50	1	US-07-828-444-8	Sequence 8, Appl1	C 474	12.8	35.6	39	5	PCT-US92-10621-79	Sequence 29, Appl
402	13	36.1	50	2	US-08-449-045C-26	Sequence 26, Appl	C 475	12.8	35.6	39	5	PCT-US94-02223-29	Sequence 29, Appl
403	13	36.1	50	1	US-08-435-605A-38	Sequence 38, Appl	476	12.8	35.6	40	2	US-08-750-810-11	Sequence 11, Appl
404	13	36.1	51	3	US-08-836-561-6	Sequence 6, Appl1	477	12.8	35.6	42	1	US-07-834-539A-30	Sequence 50, Appl
405	13	36.1	60	3	US-08-918-406-8	Sequence 8, Appl1	478	12.8	35.6	42	1	US-08-053-131-67	Sequence 67, Appl
406	13	36.1	60	6	5514646-38	Sequence 8, Appl1	479	12.8	35.6	42	1	US-08-645-641-67	Sequence 67, Appl
407	13	36.1	60	6	5514646-40	Patent No. 5514646	480	12.8	35.6	42	1	US-07-853-408B-37	Sequence 67, Appl
408	13	36.1	62	3	US-08-469-318-140	Sequence 140, App	481	12.8	35.6	42	1	US-08-096-762-67	Sequence 67, Appl
409	13	36.1	64	3	US-08-468-609A-140	Sequence 140, App	482	12.8	35.6	42	2	US-08-800-352-50	Sequence 50, Appl
410	13	36.1	64	3	US-08-875-533-27	Sequence 27, Appl	483	12.8	35.6	42	2	US-08-308-865-67	Sequence 67, Appl
411	13	36.1	64	4	PCT-US95-01185-140	Sequence 140, App	484	12.8	35.6	42	4	US-09-042-353-228	Sequence 228, App
412	13	36.1	65	1	US-08-045-806-14	Sequence 14, Appl	485	12.8	35.6	42	4	US-08-758-417A-76	Sequence 76, Appl
413	13	36.1	65	1	US-08-366-051B-14	Sequence 14, Appl	486	12.8	35.6	42	5	PCT-US92-06185-50	Sequence 50, Appl
414	13	36.1	65	4	US-09-025-769B-160	Sequence 160, App	487	12.8	35.6	42	5	PCT-US92-10983-67	Sequence 67, Appl
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416	13	36.1	69	1	US-08-484-274A-30	Sequence 30, Appl	489	12.8	35.6	44	1	US-08-672-564-7	Sequence 7, Appl1
417	13	36.1	70	2	US-08-350-260A-37	Sequence 37, Appl	C 490	12.8	35.6	44	3	US-08-726-807B-28	Sequence 28, Appl
418	13	36.1	70	2	US-09-364-380-30	Sequence 30, Appl	C 491	12.8	35.6	44	3	US-08-726-807B-30	Sequence 30, Appl
419	13	36.1	72	2	US-08-477-527A-18	Sequence 18, Appl	C 492	12.8	35.6	44	3	US-08-726-807B-41	Sequence 41, Appl
420	13	36.1	72	2	US-08-481-710-18	Sequence 18, Appl	C 493	12.8	35.6	44	3	US-08-726-807B-43	Sequence 43, Appl
421	13	36.1	72	5	PCT-US96-09537-18	Sequence 18, Appl	C 494	12.8	35.6	44	3	US-09-258-367-28	Sequence 28, Appl
422	13	36.1	72	5	US-09-522-666-20	Sequence 20, Appl	C 495	12.8	35.6	44	3	US-09-258-367-40	Sequence 40, Appl
423	13	36.1	73	4	US-08-096-947-3	Sequence 3, Appl1	C 496	12.8	35.6	44	3	US-09-258-367-41	Sequence 41, Appl
424	13	36.1	75	1	US-07-919-140B-3	Sequence 3, Appl1	C 497	12.8	35.6	44	3	US-09-258-367-43	Sequence 43, Appl
425	13	36.1	75	1	US-08-916-232-3	Sequence 3, Appl1	C 498	12.8	35.6	44	4	US-09-546-550-28	Sequence 28, Appl
426	13	36.1	75	5	PCT-US93-06939-3	Sequence 3, Appl1	C 499	12.8	35.6	44	4	US-09-546-550-30	Sequence 30, Appl
427	13	36.1	81	4	US-08-556-978B-70	Sequence 70, Appl	C 500	12.8	35.6	44	4	US-09-546-550-41	Sequence 41, Appl
428	13	36.1	81	4	US-08-483-528B-89	Sequence 89, Appl	C 501	12.8	35.6	44	4	US-09-546-550-43	Sequence 43, Appl
429	13	36.1	84	2	US-08-673-799C-89	Sequence 89, Appl	C 502	12.8	35.6	44	4	US-09-431-414-28	Sequence 28, Appl
430	13	36.1	84	2	US-08-477-527A-102	Sequence 102, App	C 503	12.8	35.6	44	4	US-09-431-414-30	Sequence 30, Appl
431	13	36.1	87	2	US-08-477-527A-171	Sequence 171, App	C 504	12.8	35.6	44	4	US-09-431-414-41	Sequence 41, Appl
432	13	36.1	87	2	US-08-481-710-102	Sequence 102, App	C 505	12.8	35.6	44	4	US-09-431-414-43	Sequence 43, Appl
433	13	36.1	87	3	US-08-481-710-102	Sequence 102, App	C 506	12.8	35.6	44	4	US-09-225-670-28	Sequence 28, Appl
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437	13	36.1	88	3	US-08-836-561-4	Sequence 4, Appl1	C 510	12.8	35.6	45	3	US-08-726-807B-49	Sequence 49, Appl
438	13	36.1	88	3	US-08-464-700-16	Sequence 16, Appl	C 511	12.8	35.6	45	3	US-09-546-550-49	Sequence 49, Appl
439	13	36.1	90	4	US-08-836-561-69	Sequence 69, Appl	C 512	12.8	35.6	45	4	US-09-431-414-49	Sequence 49, Appl
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441	13	36.1	91	3	US-08-836-561-86	Sequence 86, Appl	C 514	12.8	35.6	45	4	US-09-225-670-49	Sequence 49, Appl
442	13	36.1	91	3	US-08-836-561-86	Sequence 86, Appl	C 515	12.8	35.6	45	4	US-08-569-147-26	Sequence 26, Appl
443	13	36.1	93	1	US-08-403-762A-178	Sequence 178, App	516	12.8	35.6	47	4	US-08-569-147-28	Sequence 28, Appl
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445	13	36.1	96	3	US-08-411-098-11	Sequence 11, Appl	518	12.8	35.6	47	4	US-08-976-183A-23	Sequence 23, Appl
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448	12.8	35.6	25	3	US-08-617-454-13	Sequence 13, Appl	C 521	12.8	35.6	50	1	US-08-236-311-19	Sequence 19, Appl
449	12.8	35.6	26	3	US-08-873-437-25	Sequence 25, Appl	522	12.8	35.6	50	3	US-08-457-918-14	Sequence 14, Appl
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452	12.8	35.6	27	3	US-08-985-162-1375	Sequence 1375, Ap	C 525	12.8	35.6	55	1	US-08-674-008-18	Sequence 18, Appl
453	12.8	35.6	27	3	US-08-985-162-1543	Sequence 1543, Ap	C 526	12.8	35.6	55	6	5174993-5	Patent No. 5174993
454	12.8	35.6	27	4	US-08-584-040-353	Sequence 323, App	527	12.8	35.6	55	6	5505941-4	Patent No. 5505941
455	12.8	35.6	27	4	US-08-584-040-671	Sequence 671, App	528	12.8	35.6	56	1	US-08-171-389-600	Sequence 600, App
456	12.8	35.6	27	4	US-08-584-040-3305	Sequence 3305, Ap	529	12.8	35.6	56	1	US-08-123-936-600	Sequence 600, App
457	12.8	35.6	27	4	US-08-584-040-3385	Sequence 3385, Ap	530	12.8	35.6	56	2	US-08-472-228A-600	Sequence 600, App
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461	12.8	35.6	27	4	US-08-584-040-6801	Sequence 6801, Ap	534	12.8	35.6	59	1	US-08-413-118-50	Sequence 50, Appl
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463	12.8	35.6	30	5	US-08-722-258-22	Sequence 22, Appl	536	12.8	35.6	59	1	US-08-709-209-27	Sequence 27, Appl
464	12.8	35.6	30	5	PCT-US95-04468-22	Sequence 22, Appl	537	12.8	35.6	59	1	US-08-458-101-27	Sequence 27, Appl
465	12.8	35.6	32	3	US-08-236-886-10	Sequence 10, Appl	538	12.8	35.6	59	1		

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541	12.8	35.6	59	2	US-08-458-356-27	Sequence 27, App1	614	12.6	35.0	41	2	US-09-011-551-1	Sequence 1, App1
542	12.8	35.6	59	3	US-08-473-446-50	Sequence 50, App1	615	12.6	35.0	41	2	US-09-011-551-9	Sequence 9, App1
543	12.8	35.6	59	4	US-08-460-736-27	Sequence 27, App1	616	12.6	35.0	41	3	US-08-483-316-6	Sequence 6, App1
544	12.8	35.6	59	4	US-09-354-138-27	Sequence 27, App1	617	12.6	35.0	41	3	US-08-500-306-2	Sequence 2, App1
545	12.8	35.6	60	1	US-08-208-886C-42	Sequence 42, App1	618	12.6	35.0	41	4	US-09-262-773-172	Sequence 6, App1
546	12.8	35.6	60	1	US-08-704-744-42	Sequence 42, App1	619	12.6	35.0	41	5	PCT-US95-12624-6	Sequence 6, App1
547	12.8	35.6	60	1	US-08-469-557-42	Sequence 42, App1	620	12.6	35.0	41	6	5332671-9	Patent No. 5332671
548	12.8	35.6	60	2	US-08-290-793B-42	Sequence 42, App1	621	12.6	35.0	42	1	US-07-791-213D-49	Sequence 49, App1
549	12.8	35.6	62	2	US-08-472-171-10	Sequence 10, App1	622	12.6	35.0	42	1	US-08-256-964A-6	Sequence 6, App1
550	12.8	35.6	62	2	US-08-894-526-10	Sequence 10, App1	623	12.6	35.0	42	1	US-08-293-150A-49	Sequence 49, App1
551	12.8	35.6	62	2	US-09-013-047-10	Sequence 10, App1	624	12.6	35.0	42	3	US-08-938-830-34	Sequence 34, App1
552	12.8	35.6	62	3	US-09-374-597-10	Sequence 10, App1	625	12.6	35.0	43	4	US-09-351-814-15	Sequence 15, App1
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554	12.8	35.6	68	2	US-08-894-526-9	Sequence 9, App1	627	12.6	35.0	45	1	US-07-791-213D-48	Sequence 48, App1
555	12.8	35.0	68	3	US-09-013-047-9	Sequence 9, App1	628	12.6	35.0	45	1	US-07-972-387-72	Sequence 72, App1
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558	12.8	35.6	72	5	PCT-US96-09451-26	Sequence 26, App1	631	12.6	35.0	45	1	US-08-293-150A-48	Sequence 48, App1
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562	12.8	35.6	79	4	US-08-687-421-399	Sequence 399, App1	635	12.6	35.0	48	1	US-07-791-213D-47	Sequence 47, App1
563	12.8	35.6	90	1	US-08-220-606B-15	Sequence 15, App1	636	12.6	35.0	51	2	US-08-293-150A-47	Sequence 47, App1
564	12.8	35.6	90	1	US-08-207-901-109	Sequence 109, App1	637	12.6	35.0	51	2	US-08-850-049-35	Sequence 35, App1
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566	12.6	35.0	20	4	US-09-487-368A-179	Sequence 179, App1	639	12.6	35.0	52	4	US-09-414-117-35	Sequence 35, App1
567	12.6	35.0	21	4	US-09-398-539A-16	Sequence 16, App1	640	12.6	35.0	52	5	US-09-191-852-18	Sequence 18, App1
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570	12.6	35.0	24	1	US-08-293-150A-55	Sequence 55, App1	643	12.6	35.0	60	1	US-09-188-082-7	Sequence 7, App1
571	12.6	35.0	25	2	US-08-371-377-4	Sequence 4, App1	644	12.6	35.0	60	3	US-08-424-788B-11	Sequence 11, App1
572	12.6	35.0	26	2	US-08-859-998-21	Sequence 21, App1	645	12.6	35.0	60	3	US-08-911-894-57	Sequence 57, App1
573	12.6	35.0	26	4	US-09-225-928-21	Sequence 21, App1	646	12.6	35.0	60	4	US-09-386-281-8	Sequence 8, App1
574	12.6	35.0	27	1	US-07-791-213D-54	Sequence 54, App1	647	12.6	35.0	60	4	US-09-339-913B-27	Sequence 27, App1
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590	12.6	35.0	30	1	US-08-293-150A-53	Sequence 53, App1	663	12.6	35.0	70	2	US-08-790-963-57	Sequence 57, App1
591	12.6	35.0	31	4	US-08-679-645-358	Sequence 358, App1	664	12.6	35.0	74	1	US-09-371-774-57	Sequence 57, App1
592	12.6	35.0	31	4	US-08-679-645-365	Sequence 365, App1	665	12.6	35.0	74	1	US-08-575-361A-21	Sequence 21, App1
593	12.6	35.0	32	1	US-08-361-337-24	Sequence 24, App1	666	12.6	35.0	74	1	US-08-575-361A-22	Sequence 22, App1
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596	12.6	35.0	33	1	US-08-293-150A-52	Sequence 52, App1	669	12.6	35.0	75	1	US-08-175-155-37	Sequence 37, App1
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600	12.6	35.0	34	1	US-08-532-390-3	Sequence 3, App1	673	12.6	35.0	75	3	US-08-482-085B-73	Sequence 73, App1
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602	12.6	35.0	34	5	US-08-717-294-3	Sequence 3, App1	675	12.6	35.0	75	4	US-09-444-791A-72	Sequence 72, App1
603	12.6	35.0	34	5	PCT-US95-1511-3	Sequence 3, App1	676	12.6	35.0	80	4	US-09-444-791A-73	Sequence 73, App1
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605	12.6	35.0	35	3	US-08-462-947-11	Sequence 11, App1	678	12.6	35.0	83	3	US-09-013-872-10	Sequence 10, App1
606	12.6	35.0	36	1	US-07-791-213D-51	Sequence 51, App1	679	12.6	35.0	83	3	US-09-184-198-10	Sequence 10, App1
607	12.6	35.0	36	1	US-08-293-150A-51	Sequence 51, App1	680	12.6	35.0	86	4	US-09-338-907-109	Sequence 109, App1
608	12.6	35.0	36	3	US-09-159-374-30	Sequence 30, App1	681	12.6	35.0	86	4	US-09-218-207-109	Sequence 109, App1
609	12.6	35.0	36	3	US-09-175-837-1	Sequence 1, App1	682	12.6	35.0	87	1	US-08-403-762A-171	Sequence 171, App1
610	12.6	35.0	38	3	US-08-724-752-8	Sequence 8, App1	683	12.6	35.0	89	3	US-08-787-739-94	Sequence 94, App1
611	12.6	35.0	39	1	US-07-791-213D-50	Sequence 50, App1	684	12.6	35.0	89	4	US-09-178-115-94	Sequence 94, App1

685	12.6	35.0	89	4	US-09-177-776-94	Sequence 94, Appl	758	12.4	34.4	61	4	US-09-504-505-4	Sequence 4, Appl
C 686	12.6	35.0	90	2	US-08-483-528B-59	Sequence 59, Appl	C 759	12.4	34.4	62	3	US-09-023-228B-81	Sequence 81, Appl
C 687	12.6	35.0	90	3	US-08-673-799C-59	Sequence 59, Appl	C 760	12.4	34.4	63	2	US-08-828-008-11	Sequence 11, Appl
C 688	12.6	35.0	100	3	US-08-836-561-61	Sequence 61, Appl	761	12.4	34.4	63	4	US-08-918-148-44	Sequence 44, Appl
C 689	12.4	34.4	22	1	US-08-010-099-28	Sequence 28, Appl	762	12.4	34.4	67	3	US-08-506-553C-18	Sequence 18, Appl
C 690	12.4	34.4	22	1	US-08-140-110-3	Sequence 3, Appl	C 763	12.4	34.4	67	4	US-09-025-769B-86	Sequence 86, Appl
C 691	12.4	34.4	22	1	US-08-448-716-28	Sequence 28, Appl	C 764	12.4	34.4	69	4	US-09-025-769B-80	Sequence 80, Appl
C 692	12.4	34.4	22	4	US-09-304-186-28	Sequence 28, Appl	C 765	12.4	34.4	72	1	US-08-175-155-40	Sequence 40, Appl
C 693	12.4	34.4	23	2	US-08-332-562A-95	Sequence 95, Appl	C 766	12.4	34.4	72	1	US-08-477-509B-75	Sequence 75, Appl
C 694	12.4	34.4	23	2	US-08-332-562A-96	Sequence 96, Appl	C 767	12.4	34.4	72	2	US-08-707-237A-66	Sequence 46, Appl
C 695	12.4	34.4	24	1	US-08-392-828C-22	Sequence 22, Appl	C 768	12.4	34.4	72	3	US-08-482-085B-75	Sequence 75, Appl
C 696	12.4	34.4	24	3	US-09-330-945-22	Sequence 22, Appl	C 769	12.4	34.4	72	4	US-09-444-791A-75	Sequence 75, Appl
C 697	12.4	34.4	24	5	PCT-US95-08493-11	Sequence 11, Appl	C 770	12.4	34.4	73	4	US-08-584-760A-10	Sequence 10, Appl
C 698	12.4	34.4	27	3	US-08-758-306-674	Sequence 674, Appl	C 771	12.4	34.4	77	1	US-08-400-440A-73	Sequence 23, Appl
C 699	12.4	34.4	27	3	US-09-257-799-44	Sequence 44, Appl	C 772	12.4	34.4	77	1	US-08-463-003A-23	Sequence 23, Appl
C 700	12.4	34.4	27	3	US-08-985-162-946	Sequence 946, App	C 773	12.4	34.4	77	2	US-08-460-888A-23	Sequence 23, Appl
C 701	12.4	34.4	27	3	US-08-920-919A-44	Sequence 44, Appl	C 774	12.4	34.4	77	2	US-08-894-578-88	Sequence 23, Appl
C 702	12.4	34.4	27	4	US-08-584-040-3318	Sequence 3318, Ap	C 775	12.4	34.4	77	4	US-09-320-424-18	Sequence 18, Appl
C 703	12.4	34.4	27	4	US-08-584-040-6906	Sequence 6906, Ap	C 776	12.4	34.4	77	4	US-09-412-017-23	Sequence 23, Appl
C 704	12.4	34.4	29	2	US-08-415-593-13	Sequence 13, Appl	C 777	12.4	34.4	78	2	US-08-477-527A-224	Sequence 224, App
C 705	12.4	34.4	30	1	US-08-428-370A-8	Sequence 8, Appl	C 778	12.4	34.4	78	3	US-08-481-710-224	Sequence 224, App
C 706	12.4	34.4	30	1	US-08-463-975-4	Sequence 4, Appl	C 779	12.4	34.4	78	5	PCT-US96-09537-224	Sequence 224, App
C 707	12.4	34.4	30	1	US-08-783-266-4	Sequence 4, Appl	C 780	12.4	34.4	79	4	US-08-584-760A-21	Sequence 21, Appl
C 708	12.4	34.4	30	2	US-08-600-766-8	Sequence 8, Appl	C 781	12.4	34.4	81	4	US-09-133-321-7	Sequence 7, Appl
C 709	12.4	34.4	30	2	US-09-023-321-4	Sequence 4, Appl	C 782	12.4	34.4	84	1	US-08-209-747-50	Sequence 50, Appl
C 710	12.4	34.4	30	4	US-09-042-353-5	Sequence 5, Appl	C 783	12.4	34.4	84	1	US-08-458-298-50	Sequence 50, Appl
C 711	12.4	34.4	30	4	US-08-758-417A-773	Sequence 273, App	C 784	12.4	34.4	87	4	US-08-556-978B-56	Sequence 56, Appl
C 712	12.4	34.4	31	4	US-08-679-645-333	Sequence 333, App	C 785	12.4	34.4	87	4	US-08-556-978B-57	Sequence 57, Appl
C 713	12.4	34.4	33	2	US-08-407-900B-1	Sequence 1, Appl	C 786	12.4	34.4	90	4	US-08-974-549A-671	Sequence 671, App
C 714	12.4	34.4	33	2	US-08-411-607A-9	Sequence 9, Appl	C 787	12.4	34.4	90	4	US-08-974-549A-672	Sequence 672, App
C 715	12.4	34.4	33	3	US-08-379-802-10	Sequence 10, Appl	C 788	12.4	34.4	96	2	US-08-436-664-18	Sequence 18, Appl
C 716	12.4	34.4	33	3	US-09-048-129-10	Sequence 10, Appl	C 789	12.4	34.4	96	3	US-09-135-642-18	Sequence 18, Appl
C 717	12.4	34.4	33	4	US-09-048-079-10	Sequence 10, Appl	C 790	12.4	34.4	96	3	US-08-394-232A-18	Sequence 18, Appl
C 718	12.4	34.4	33	4	US-09-370-961-1	Sequence 1, Appl	C 791	12.4	34.4	96	5	PCT-US95-04080-18	Sequence 18, Appl
C 719	12.4	34.4	36	4	US-08-994-962-8	Sequence 8, Appl	C 792	12.4	34.4	99	3	US-09-070-842A-2	Sequence 2, Appl
C 720	12.4	34.4	36	4	US-08-943-136-17	Sequence 17, Appl	C 793	12.2	33.9	17	2	US-08-293-620A-1701	Sequence 1701, Ap
C 721	12.4	34.4	36	4	US-08-973-518-17	Sequence 17, Appl	C 794	12.2	33.9	17	3	US-09-071-845-1701	Sequence 1701, Ap
C 722	12.4	34.4	37	3	US-08-968-563-21	Sequence 21, Appl	C 795	12.2	33.9	18	2	US-08-154-146-10	Sequence 10, Appl
C 723	12.4	34.4	37	3	US-08-964-268-11	Sequence 14, Appl	C 796	12.2	33.9	18	2	US-09-154-344-10	Sequence 10, Appl
C 724	12.4	34.4	37	3	US-08-969-683A-21	Sequence 21, Appl	C 797	12.2	33.9	19	3	US-08-332-166A-95	Sequence 95, Appl
C 725	12.4	34.4	37	3	US-08-969-683A-51	Sequence 51, Appl	C 798	12.2	33.9	19	4	US-09-326-166B-95	Sequence 95, Appl
C 726	12.4	34.4	40	2	US-08-411-607A-7	Sequence 7, Appl	C 799	12.2	33.9	20	3	US-09-484-345-17	Sequence 17, Appl
C 727	12.4	34.4	41	1	US-08-644-271-24	Sequence 24, Appl	C 800	12.2	33.9	20	4	US-09-487-368A-52	Sequence 52, Appl
C 728	12.4	34.4	41	1	US-08-718-738-5	Sequence 5, Appl	C 801	12.2	33.9	20	5	PCT-US95-11405-26	Sequence 26, Appl
C 729	12.4	34.4	41	4	US-08-961-810-97	Sequence 97, Appl	C 802	12.2	33.9	21	3	US-09-357-746-13	Sequence 13, Appl
C 730	12.4	34.4	41	4	US-08-352-902D-97	Sequence 97, Appl	C 803	12.2	33.9	21	4	US-08-930-264-31	Sequence 31, Appl
C 731	12.4	34.4	41	4	US-09-221-844-5	Sequence 5, Appl	C 804	12.2	33.9	21	4	US-08-811-463-21	Sequence 21, Appl
C 732	12.4	34.4	41	5	PCT-US95-03323A-5	Sequence 5, Appl	C 805	12.2	33.9	21	4	US-08-811-463-21	Sequence 21, Appl
C 733	12.4	34.4	42	2	US-08-716-284-3	Sequence 3, Appl	C 806	12.2	33.9	21	4	US-09-228-324A-53	Sequence 53, Appl
C 734	12.4	34.4	44	2	US-08-350-260A-166	Sequence 166, App	C 807	12.2	33.9	21	5	PCT-US95-11405-27	Sequence 27, Appl
C 735	12.4	34.4	47	4	US-09-338-907-280	Sequence 280, App	C 808	12.2	33.9	22	1	US-08-235-180-18	Sequence 18, Appl
C 736	12.4	34.4	47	4	US-09-218-207-280	Sequence 280, App	C 809	12.2	33.9	22	1	US-08-332-160-24	Sequence 24, Appl
C 737	12.4	34.4	48	3	US-08-911-894-61	Sequence 61, Appl	C 810	12.2	33.9	22	3	US-08-974-180-2	Sequence 2, Appl
C 738	12.4	34.4	49	1	US-07-994-469A-43	Sequence 43, Appl	C 811	12.2	33.9	22	3	US-08-777-266B-94	Sequence 94, Appl
C 739	12.4	34.4	50	2	US-08-850-049-8	Sequence 8, Appl	C 812	12.2	33.9	22	4	US-09-326-166B-94	Sequence 94, Appl
C 740	12.4	34.4	50	2	US-08-050-478-8	Sequence 8, Appl	C 813	12.2	33.9	23	4	US-08-781-891-128	Sequence 128, App
C 741	12.4	34.4	50	4	US-07-858-747B-8	Sequence 8, Appl	C 814	12.2	33.9	24	3	US-08-777-266A-93	Sequence 93, Appl
C 742	12.4	34.4	50	4	US-09-091-814-50	Sequence 50, Appl	C 815	12.2	33.9	24	4	US-09-326-166B-93	Sequence 93, Appl
C 743	12.4	34.4	50	4	US-09-414-117-8	Sequence 8, Appl	C 816	12.2	33.9	25	3	US-08-911-894-41	Sequence 41, Appl
C 744	12.4	34.4	53	1	US-08-429-181-50	Sequence 50, Appl	C 817	12.2	33.9	25	4	US-09-194-285-17	Sequence 17, Appl
C 745	12.4	34.4	53	1	US-08-164-388-50	Sequence 50, Appl	C 818	12.2	33.9	26	2	US-08-508-553B-9	Sequence 9, Appl
C 746	12.4	34.4	55	3	US-08-911-894-63	Sequence 63, Appl	C 819	12.2	33.9	26	2	US-08-908-005A-9	Sequence 9, Appl
C 747	12.4	34.4	56	4	US-09-091-814-49	Sequence 49, Appl	C 820	12.2	33.9	26	4	US-09-253-523-9	Sequence 9, Appl
C 748	12.4	34.4	60	3	US-08-911-894-56	Sequence 56, Appl	C 821	12.2	33.9	26	4	US-09-251-911-9	Sequence 9, Appl
C 749	12.4	34.4	60	3	US-08-911-894-65	Sequence 65, Appl	C 822	12.2	33.9	27	2	US-08-284-941-13	Sequence 13, Appl
C 750	12.4	34.4	61	1	US-07-910-222B-4	Sequence 4, Appl	C 823	12.2	33.9	27	2	US-08-948-132-1	Sequence 1, Appl
C 751	12.4	34.4	61	1	US-08-070-158-4	Sequence 4, Appl	C 824	12.2	33.9	27	2	US-08-447-642-13	Sequence 13, Appl
C 752	12.4	34.4	61	1	US-08-200-716-4	Sequence 4, Appl	C 825	12.2	33.9	27	3	US-08-985-162-86	Sequence 86, App
C 753	12.4	34.4	61	3	US-08-015-147-4	Sequence 4, Appl	C 826	12.2	33.9	27	4	US-09-236-503-13	Sequence 13, Appl
C 754	12.4	34.4	61	3	US-08-469-015-4	Sequence 4, Appl	C 827	12.2	33.9	27	4	US-08-584-040-177	Sequence 177, App
C 755	12.4	34.4	61	3	US-08-463-893-4	Sequence 4, Appl	C 828	12.2	33.9	27	4	US-08-584-040-640	Sequence 640, App
C 756	12.4	34.4	61	3	US-08-506-553C-17	Sequence 17, Appl	C 829	12.2	33.9	27	4	US-08-584-040-3162	Sequence 3162, Ap
C 757	12.4	34.4	61	4	US-08-891-292A-77	Sequence 77, Appl	C 830	12.2	33.9	27	4	US-08-584-040-3687	Sequence 3687, Ap



C 831	12.2	33.9	27	4	US-08-584-040-4725	Sequence 4725, Ap	904	12.2	33.9	43	3	US-08-673-799C-22	Sequence 22, Appl
C 832	12.2	33.9	27	4	US-08-584-040-5091	Sequence 5091, Ap	905	12.2	33.9	43	4	US-09-351-814-21	Sequence 21, Appl
C 833	12.2	33.9	27	4	US-08-584-040-5092	Sequence 5092, Ap	906	12.2	33.9	44	4	US-08-569-151-77-29	Sequence 29, Appl
C 834	12.2	33.9	27	4	US-08-584-040-6380	Sequence 6380, Ap	907	12.2	33.9	44	4	US-08-976-183A-24	Sequence 24, Appl
C 835	12.2	33.9	27	5	PCT-US93-02147A-13	Sequence 13, Appl	908	12.2	33.9	45	1	US-08-411-796-72	Sequence 72, Appl
C 836	12.2	33.9	28	1	US-08-403-762A-72	Sequence 72, Appl	909	12.2	33.9	45	1	US-08-411-796-72	Sequence 72, Appl
C 837	12.2	33.9	28	3	US-08-968-563-40	Sequence 40, Appl	910	12.2	33.9	45	3	US-08-471-039-72	Sequence 72, Appl
C 838	12.2	33.9	28	3	US-08-969-683A-40	Sequence 40, Appl	911	12.2	33.9	45	3	US-08-471-039-72	Sequence 72, Appl
C 839	12.2	33.9	30	1	US-07-938-084-19	Sequence 19, Appl	912	12.2	33.9	45	4	US-08-647-924-15	Sequence 2, Appl
C 840	12.2	33.9	30	1	US-08-479-487-34	Sequence 34, Appl	913	12.2	33.9	45	4	US-09-091-814-15	Sequence 15, Appl
C 841	12.2	33.9	30	5	PCT-US93-07672-1	Sequence 1, Appl	914	12.2	33.9	45	4	US-09-199-737-43	Sequence 43, Appl
C 842	12.2	33.9	31	2	US-08-483-528B-12	Sequence 12, Appl	915	12.2	33.9	45	4	US-09-199-737-44	Sequence 44, Appl
C 843	12.2	33.9	31	3	US-08-673-799C-12	Sequence 12, Appl	916	12.2	33.9	45	4	US-09-425-638A-13	Sequence 13, Appl
C 844	12.2	33.9	32	1	US-08-889-502-12	Sequence 12, Appl	917	12.2	33.9	45	4	US-09-543-004-13	Sequence 13, Appl
C 845	12.2	33.9	33	1	US-08-398-613A-26	Sequence 26, Appl	918	12.2	33.9	45	5	PCT-US93-11198-72	Sequence 72, Appl
C 846	12.2	33.9	33	1	US-08-398-612A-26	Sequence 26, Appl	919	12.2	33.9	45	5	PCT-US93-11198-237	Sequence 237, App
C 847	12.2	33.9	33	1	US-08-398-611A-26	Sequence 26, Appl	920	12.2	33.9	46	2	US-08-652-558-28	Sequence 28, Appl
C 848	12.2	33.9	33	1	US-08-396-851A-26	Sequence 26, Appl	921	12.2	33.9	46	4	US-08-569-147-49	Sequence 49, Appl
C 849	12.2	33.9	33	1	US-08-491-334A-26	Sequence 26, Appl	922	12.2	33.9	47	1	US-08-466-852-2	Sequence 2, Appl
C 850	12.2	33.9	33	2	US-09-027-449-23	Sequence 23, Appl	923	12.2	33.9	48	4	US-09-425-638A-38	Sequence 38, Appl
C 851	12.2	33.9	33	3	US-08-804-444A-23	Sequence 23, Appl	924	12.2	33.9	48	4	US-09-543-004-38	Sequence 38, Appl
C 852	12.2	33.9	33	3	US-09-026-985-23	Sequence 23, Appl	925	12.2	33.9	49	5	PCT-US92-10430-16	Sequence 16, Appl
C 853	12.2	33.9	34	3	US-08-477-460B-7	Sequence 7, Appl	926	12.2	33.9	49	5	PCT-US93-11638-7	Sequence 7, Appl
C 854	12.2	33.9	34	3	US-08-379-516-7	Sequence 7, Appl	927	12.2	33.9	50	4	US-08-569-147-24	Sequence 24, Appl
C 855	12.2	33.9	34	4	US-09-329-916-7	Sequence 7, Appl	928	12.2	33.9	50	4	US-08-976-183A-19	Sequence 19, Appl
C 856	12.2	33.9	34	4	US-08-485-372A-7	Sequence 7, Appl	929	12.2	33.9	50	4	US-09-260-038B-12	Sequence 12, Appl
C 857	12.2	33.9	34	4	US-09-409-006A-7	Sequence 7, Appl	930	12.2	33.9	52	4	US-08-943-136-19	Sequence 19, Appl
C 858	12.2	33.9	34	5	PCT-US93-07422-7	Sequence 7, Appl	931	12.2	33.9	52	4	US-08-973-518-19	Sequence 19, Appl
C 859	12.2	33.9	35	2	US-08-116-778E-29	Sequence 29, Appl	932	12.2	33.9	52	4	US-09-260-038B-11	Sequence 11, Appl
C 860	12.2	33.9	35	2	US-08-438-562-29	Sequence 29, Appl	933	12.2	33.9	53	4	US-09-260-038B-10	Sequence 10, Appl
C 861	12.2	33.9	35	2	US-08-910-731-13	Sequence 13, Appl	934	12.2	33.9	54	1	US-08-468-674B-65	Sequence 65, Appl
C 862	12.2	33.9	35	2	US-08-483-528B-29	Sequence 29, Appl	935	12.2	33.9	54	1	US-08-760-571-65	Sequence 65, Appl
C 863	12.2	33.9	35	3	US-08-673-799C-29	Sequence 29, Appl	936	12.2	33.9	55	2	US-08-330-394A-27	Sequence 27, Appl
C 864	12.2	33.9	35	3	US-08-661-083-450	Sequence 450, App	937	12.2	33.9	55	5	PCT-US92-10024-3	Sequence 3, Appl
C 865	12.2	33.9	36	1	US-08-151-574-26	Sequence 26, Appl	938	12.2	33.9	55	5	PCT-US92-10024-4	Sequence 4, Appl
C 866	12.2	33.9	36	1	US-08-912-976-6	Sequence 6, Appl	939	12.2	33.9	56	1	US-08-468-674B-31	Sequence 31, Appl
C 867	12.2	33.9	36	2	US-08-419-448-26	Sequence 26, Appl	940	12.2	33.9	56	1	US-08-780-571-31	Sequence 31, Appl
C 868	12.2	33.9	36	4	US-09-233-510-26	Sequence 26, Appl	941	12.2	33.9	56	2	US-08-330-394A-28	Sequence 28, Appl
C 869	12.2	33.9	37	1	US-08-285-936-20	Sequence 20, Appl	942	12.2	33.9	56	4	US-09-091-814-57	Sequence 57, Appl
C 870	12.2	33.9	37	1	US-08-360-125-1	Sequence 1, Appl	943	12.2	33.9	57	3	US-08-888-381-7	Sequence 7, Appl
C 871	12.2	33.9	37	1	US-08-487-860-20	Sequence 20, Appl	944	12.2	33.9	58	2	US-08-883-795A-6	Sequence 6, Appl
C 872	12.2	33.9	37	1	US-08-485-721-24	Sequence 24, Appl	945	12.2	33.9	58	2	US-08-883-795A-22	Sequence 22, Appl
C 873	12.2	33.9	37	2	US-08-450-578-1	Sequence 1, Appl	946	12.2	33.9	59	1	US-08-208-886C-26	Sequence 26, Appl
C 874	12.2	33.9	37	2	US-08-392-935-24	Sequence 24, Appl	947	12.2	33.9	59	1	US-08-704-744-26	Sequence 26, Appl
C 875	12.2	33.9	37	2	US-09-017-628-1	Sequence 1, Appl	948	12.2	33.9	59	1	US-08-469-557-26	Sequence 26, Appl
C 876	12.2	33.9	37	2	US-09-014-880-1	Sequence 1, Appl	949	12.2	33.9	59	2	US-08-280-793B-26	Sequence 26, Appl
C 877	12.2	33.9	37	3	US-08-810-720-6	Sequence 6, Appl	950	12.2	33.9	59	4	US-09-260-038B-9	Sequence 9, Appl
C 878	12.2	33.9	37	3	US-08-857-236-9	Sequence 9, Appl	951	12.2	33.9	60	1	US-08-374-641-5	Sequence 5, Appl
C 879	12.2	33.9	37	4	US-09-167-874-9	Sequence 9, Appl	952	12.2	33.9	63	1	US-08-198-431-32	Sequence 32, Appl
C 880	12.2	33.9	37	4	US-08-590-563-13	Sequence 13, Appl	953	12.2	33.9	63	1	US-08-564-955-32	Sequence 32, Appl
C 881	12.2	33.9	37	5	PCT-US93-08326-24	Sequence 24, Appl	954	12.2	33.9	63	2	US-08-537-874-32	Sequence 32, Appl
C 882	12.2	33.9	38	4	US-09-224-014-3	Sequence 3, Appl	955	12.2	33.9	63	3	US-08-828-009-11	Sequence 11, Appl
C 883	12.2	33.9	40	1	US-07-938-084-13	Sequence 13, Appl	956	12.2	33.9	63	3	US-08-621-859-32	Sequence 32, Appl
C 884	12.2	33.9	40	1	US-08-411-796-71	Sequence 71, Appl	957	12.2	33.9	63	3	US-09-100-856A-32	Sequence 32, Appl
C 885	12.2	33.9	40	1	US-08-411-796-236	Sequence 236, App	958	12.2	33.9	63	4	US-09-075-511-32	Sequence 32, Appl
C 886	12.2	33.9	40	1	US-08-857-946-49	Sequence 49, Appl	959	12.2	33.9	63	4	US-09-099-015-32	Sequence 32, Appl
C 887	12.2	33.9	40	3	US-08-827-336-3	Sequence 3, Appl	960	12.2	33.9	63	4	US-09-232-863-32	Sequence 32, Appl
C 888	12.2	33.9	40	3	US-08-970-730-49	Sequence 49, Appl	961	12.2	33.9	63	4	US-09-133-508A-32	Sequence 32, Appl
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## ALIGNMENTS

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RESULT 1
US-08-765-783A-30
; Sequence 30, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; APPLICATION NUMBER: US/08/765.783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..34
; OTHER INFORMATION: chvL backward primer
; US-08-765-783A-30

Query Match 53.3%; Score 19.2; DB 2; Length 34;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 aaagcttcaccatgacgacgacccaagt 35
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Db 3 AAAGCTTCACCATGAGTGTCTCAGTCAGGT 34
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; Sequence 30, Application us/08921100
; Patent No. 6024956
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATSUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921.100
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,323
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-921-100-30

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Best Local Similarity 75.0%; Pred. No. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 3 AAAGCTTCACCATGAGTGTCTCAGT 34

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; Sequence 30, Application US/08880142  
; Patent No. 6048972  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATSUMI  
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; City: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
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; SOFTWARE: Patentin Release #1.0, Version #1.30  
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; FILING DATE: 20-JUN-1997  
; CLASSIFICATION: 536  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/345,145  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-880-142-30

Query Match 53.3%; Score 19.2; DB 3; Length 34;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 3 AAAGCTTCACCATGAGTGTCTCAGT 34

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US-08-902-201-30  
; Sequence 30, Application US/08902201  
; Patent No. 6068840  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATSUMI

; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; City: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,201  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 424  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/437,328  
; FILING DATE: 09-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-902-201-30

Query Match 53.3%; Score 19.2; DB 3; Length 34;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 3 AAAGCTTCACCATGAGTGTCTCAGT 34

RESULT 5  
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; Sequence 30, Application US/09416557  
; Patent No. 6245894  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATSUMI  
; TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; City: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/416,557
3 FILING DATE: 12-October-1999
4 CLASSIFICATION:
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/765,783
7 FILING DATE: 7-March-1997
8 ATTORNEY/AGENT INFORMATION:
9 NAME: Murashige, Kate H
10 REGISTRATION NUMBER: 29,959
11 REFERENCE/DOCKET NUMBER: 35029-20001.10
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 202-887-1500
14 TELEFAX: 202-822-0168
15 TELEX:
16 INFORMATION FOR SEQ ID NO: 30:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 34 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 FEATURE:
23 NAME/KEY: Other
24 LOCATION: 1...34
25 OTHER INFORMATION: chvL backward primer
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Query Match	53.3%	Score 19.2	DB 4	Length 34
Best Local Similarity	75.0%	Pred. No. 27		
Matches 24; Conservative	0	Mismatches 8	Indels 0	Gaps 0

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db      3 AAAGCTTCACCATGAGTGTGCTCACTCAGGT 34

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RESULT 6  
 US-08-424-424B-5  
 Sequence 5, Application US/08424424B  
 Patent No. 5739834  
 GENERAL INFORMATION:  
 APPLICANT: LI, ET AL.  
 TITLE OF INVENTION: Neurotransmitter Transporter  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,424B  
 FILING DATE: APRIL 21, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/05363  
 FILING DATE: MAY 25, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J.G.  
 REGISTRATION NUMBER: 33,073  
 REFERENCE/DOCKET NUMBER: 325800-308  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 BASE PAIRS
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: SINGLE
;     TOPOLOGY: LINEAR
;     MOLECULE TYPE: Oligonucleotide
US-08-424-424B-5

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Query Match	51.7%;	Score 18.6;	DB 1;	Length 38;
Best Local Similarity	72.7%;	Pred. No. 47;		
Matches 24; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

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QY      4 aaagcttcaccatgagccaggaacaccaaagtg 36
          | | | | | | | | | | | | | | | |
Db      6 AGATCTGCCACCATGCCGAGAGACAGCAAGTG 38
```

RESULT 7  
US-08-483-511-14  
Sequence 14, Application US/08483511  
Patent No. 6297048  
GENERAL INFORMATION:  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Lee, William T.L.  
APPLICANT: Townsend, Kay  
APPLICANT: O'Dea, Joanne  
TITLE OF INVENTION: HEPATITIS THERAPEUTICS  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:

Query Match	51.7%	Score 18.6	DB 4	Length 55
Best Local Similarity	72.7%	Pred. No. 49		
Matches 24	Conservative 0	Mismatches 9	Indels 0	Gaps 0

QY 1 gcgaagcttcaccatgagccagycaccca aa 33  
||| ||||||||| | |||  
Db 3 GCTTAAGCTTCCACCATGAGCACAATA TCCTAA 35

## RESULT 8



REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-127-721A-24

Query Match 50.0%; Score 18; DB 3; Length 82;  
Best Local Similarity 80.8%; Pred. No. 89;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 ccacatgagcagacagaccagaagt 36  
||||| | ||||| | ||||| | ||  
Db 60 CCACCTTCGCGCAGGCGCACCAGGTG 35

RESULT 11  
US-08-485-246A-24/C  
Sequence 24, Application US/08485246A  
Patent No. 6072035  
GENERAL INFORMATION:  
APPLICANT: Hardman, No. 6072035man  
APPLICANT: Kolbinger, Frank  
APPLICANT: Saldanha, Jose  
TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6072035artis Patent Department  
STREET: 59 Route 10  
CITY: East Hanover  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07936-1080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,246A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/127,721  
FILING DATE: 27-SEPTEMBER-1993  
APPLICATION NUMBER: US 07/952,802  
FILING DATE: 25-SEPTEMBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6072035ak, Henry P.  
REGISTRATION NUMBER: 33,200  
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-485-246A-24

Query Match 50.0%; Score 18; DB 3; Length 82;

Best Local Similarity 80.8%; Pred. No. 89;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 11 ccacatgagcagacagaccagaagt 36  
||||| | ||||| | ||||| | ||  
Db 60 CCACCTTCGCGCAGGCGCACCAGGTG 35

RESULT 12  
US-07-969-931-25  
Sequence 25, Application US/07969931  
Patent No. 5458874  
GENERAL INFORMATION:  
APPLICANT: Pereira, Heloise Anne  
APPLICANT: Spitznagel, John K.  
TITLE OF INVENTION: Chemotactic, Antibiotic and  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Needle & Rosenberg, P.C.  
STREET: 133 Carnegie Way N.W., Suite 400  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,931  
FILING DATE: 19921030  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/543,151  
FILING DATE: 25-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/375,739  
FILING DATE: 05-JUL-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Severson, Mary L.  
REGISTRATION NUMBER: 34,927  
REFERENCE/DOCKET NUMBER: 0510.024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-969-931-25

Query Match 47.2%; Score 17; DB 1; Length 43;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 aagcttcacatgagcagacac 29  
||||| | ||||| | ||||| | ||  
Db 11 AAGCTTCACATGAGCCGCGTGAC 35

RESULT 13  
US-07-855-417A-25  
Sequence 25, Application US/07855417A  
Patent No. 5484885  
GENERAL INFORMATION:  
APPLICANT: Pereira, Heloise Anne  
APPLICANT: Spitznagel, John K.

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/479,783A
3 FILING DATE: 7-JUNE-1995
4 CLASSIFICATION: 536
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 07/714,131
7 FILING DATE: 10-JUNE-1991
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 07/931,473
10 FILING DATE: 17-AUGUST-1992
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 07/964,624
13 FILING DATE: 21-OCTOBER-1992
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 08/117,991
16 FILING DATE: 8-SEPTEMBER-1993
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 07/536,428
19 FILING DATE: 11-JUNE-1990
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Diane H. McLearn
22 REGISTRATION NUMBER: 33,960
23 REFERENCE/DOCKET NUMBER: NEXA2-2
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (303) 793-3333
26 TELEFAX: (303) 793-4433
27 INFORMATION FOR SEO ID NO: 57:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 96 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: RNA
34 FEATURE:
35 OTHER INFORMATION: All pyrimidines are 2'-F
36 OTHER INFORMATION: modified
37
38 US-08-479-783A-57

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Query Match	47.2%	Score 17	DB 1	Length 96
Best Local Similarity	68.0%	Pred. No. 2.3e+02		
Matches	17	Conservative	3	Mismatches 5
				Indels 0
				Gaps 0
OY	3	gaagctccaccatgacgcagac	27	
db	41	gacacccuuuagccavagacugcgac	65	

RESULT 15  
US-08-479-725-57  
Sequence 57, Application US/08479725  
Patent No. 5674685  
GENERAL INFORMATION:  
APPLICANT: NEBOJSA JANJIC  
APPLICANT: LARRY GOLD  
TITLE OF INVENTION: HIGH AFFINITY PGCF NUCLEIC  
TITLE OF INVENTION: ACID LIGANDS  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson and Bratschun, L.L.C.  
STREET: 8400 East Prentice Avenue, Suite #200  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,725  
FILING DATE: 7-JUNE-1995

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1 CLASSIFICATION: 536
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 07/714,131
4 FILING DATE: 10-JUNE-1991
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 07/931,473
7 FILING DATE: 17-AUGUST-1992
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 07/966,624
10 FILING DATE: 21-OCTOBER-1992
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 08/117,991
13 FILING DATE: 8-SEPTEMBER-1993
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 07/536,428
16 FILING DATE: 11-JUNE-1990
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Diane H. McClearn
19 REGISTRATION NUMBER: 33,960
20 REFERENCE/DOCKET NUMBER: NEXA2-1
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (303) 793-3433
23 TELEFAX: (303) 793-3433
24 INFORMATION FOR SEQ. ID NO: 57:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 96 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: RNA
31 FEATURE:
32 OTHER INFORMATION: All pyrimidines are 2'-F
33
34 OS-08-479-725-57

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Query March	47.2%	Score 17	DB 1	Length 96
Best Local Similarity	68.0%	Pred. No. 2.3e+02		
Matches 17, Conservative	3	Mismatches 5	Indels 0	Gaps 0
QY	3	gaagcttcacacatgagccagac	27	
db	41	gacacuuuagcccaugacucggac	65	

Search completed: June 22, 2002, 05:33:31  
Job time: 4741 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:05:40 ; Search time 2443.9 Seconds  
(without alignments)  
198.818 Million cell updates/sec

Title: US-09-927-267-12  
Perfect score: 36  
Sequence: 1 gcgaagctccacatgagcagcagcacaagt 36

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estln: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pln: \*  
16: em\_gss\_vrc: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	48.9	61	10	BE571706
2	17.6	48.9	64	10	AA256029
3	17.4	48.3	70	12	TA386B040
4	17.4	48.3	77	9	AI158677
5	16.8	46.7	58	9	AI023530
6	16.8	46.7	66	12	A2328396
7	16	44.4	62	10	F24048
8	16	44.4	62	12	CNS03D7C
9	16	44.4	85	12	A2920865
10	16	44.4	93	9	AA062074
11	15.8	43.9	71	12	A2499552
12	15.8	43.3	80	10	R46756
13	15.6	43.3	43	10	BI197684
14	15.6	43.3	43	10	BF311795
15	15.6	43.3	43	10	BF312493
16	15.6	43.3	43	10	BF315164
17	15.6	43.3	70	10	BG503868

18	15.6	43.3	73	10	BE228766
19	15.6	43.3	74	12	BH226010
20	15.6	43.3	79	9	AA587583
21	15.4	42.8	63	9	AV833733
22	15.4	42.8	70	9	AI089535
23	15.4	42.8	78	9	AA674932
24	15.4	42.8	84	9	AA113951
25	15.4	42.8	95	10	BF718449
26	15.2	42.2	64	9	AA013549
27	15.2	42.2	82	9	AI679682
28	15.2	42.2	94	12	BSA275789
29	15.2	42.2	96	9	AM307064
30	15.2	42.2	98	10	T61786
31	15.2	42.2	100	12	T81604
32	15.2	42.2	100	12	A2785459
33	15.2	41.7	43	12	A2411328
34	15.2	41.7	55	10	BI091807
35	15.2	41.7	79	12	BI091807
36	15.2	41.7	85	9	AI545056
37	15.2	41.7	85	10	T60481
38	15.2	41.7	92	10	D12094
39	15.2	41.7	96	9	AI414856
40	15.2	41.7	97	9	AA633275
41	15.2	41.7	98	9	AA874106
42	15.2	41.7	98	10	BI862877
43	15.2	41.7	100	10	BF946786
44	14.8	41.1	34	9	AA779194
45	14.8	41.1	49	10	BE282036
46	14.8	41.1	60	12	A2609301
47	14.8	41.1	69	9	AA551533
48	14.8	41.1	73	9	AA934094
49	14.8	41.1	73	10	WA83192
50	14.8	41.1	73	12	TA61B09P
51	14.8	41.1	74	9	AA246231
52	14.8	41.1	79	9	AA731299
53	14.8	41.1	80	10	D19080
54	14.8	41.1	83	9	AA532978
55	14.8	41.1	87	12	AA230176
56	14.8	41.1	87	12	A2600429
57	14.8	41.1	88	10	F37888
58	14.8	41.1	88	12	A2788938
59	14.8	41.1	89	10	BM284162
60	14.8	41.1	91	9	AA077122
61	14.8	41.1	93	10	H86708
62	14.8	41.1	96	9	AI955343
63	14.8	41.1	100	10	BG209819
64	14.6	40.6	35	12	A2763763
65	14.6	40.6	35	12	A2767591
66	14.6	40.6	37	12	A2417824
67	14.6	40.6	46	12	A2793780
68	14.6	40.6	54	12	A2796113
69	14.6	40.6	72	10	BG151288
70	14.6	40.6	76	10	H53922
71	14.6	40.6	81	10	BE891840
72	14.6	40.6	82	10	T60383
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74	14.6	40.6	91	12	AI957617
75	14.6	40.6	92	12	A2606696
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77	14.6	40.6	96	9	AA458451
78	14.6	40.6	98	9	AA026309
79	14.4	40.0	48	10	N57213
80	14.4	40.0	51	12	A2808470
81	14.4	40.0	53	9	AV852307
82	14.4	40.0	53	10	BG235568
83	14.4	40.0	55	10	BG231022
84	14.4	40.0	60	10	BG271430
85	14.4	40.0	61	10	W95439
86	14.4	40.0	69	9	AA930101
87	14.4	40.0	73	9	AA191061
88	14.4	40.0	77	2	HSM003312
89	14.4	40.0	78	10	T74784
90	14.4	40.0	79	12	A24742270

BE228766	SMOVL3CAN
BH226010	1006129F0
AA587583	nd44C04.r
AV833733	AV833733
AI089535	qa07a02.x
AA674932	vq51f05.r
AA113951	zm81C10.r
BF718449	EST222.m1
AA013549	mh10e04.r
AI679682	lu55d02.x
AJ275789	Homo sapi
AM307064	s152d02.y
T61786	yb93h07.r1
T81604	yD30a11.r1
A2785459	2M0029B21
A2411328	1M0184P17
BI091807	60285866
B31794	HS-1012-B1-
AI545056	fb70b05.y
T60481	yb95d04.s1
D12094	HUM0516B10
AI414856	mb49b10.x
AA633275	nq58b09.s
AA874106	vw8f08.r
BI862877	rm13e04.y
BF946786	CM2-NN021
AA779194	z51b04.s
BE282036	601102010
A2609301	1M0434C04
AA551533	L008C08-
AA934094	On39d02.s
WA83192	mf09d05.r1
AI456614	T. brucei
AA246231	2821727.s
AA731299	nw66g05.s
D19080	MUSGS01287
AA532978	n19a06.s
AA230176	up26f11.y
A2600429	1M0418D15
F37888	HSPD07215.H
A2788938	2M0035E20
BM284162	K130904.Y
AA077122	7B08C08.C
H86708	yt06h05.s1
AI955343	w11a05.x
BG209819	RSF29346
A2763763	1M0559D21
A2767591	2M0034B12
A2417824	1M0193I07
A2793780	2M0047C17
A2796113	2M0051M03
BG151288	na136a02.
H53922	yq87g04.r1
BE891840	601434286
T60383	yb93b12.r1
A2787015	2M0032A20
AI957617	fc95g05.x
A2606696	1M0428D17
BG231012	na143C05.
AA458451	vf88h11.r
AA026309	ze97c06.r
NS7213	yw65b02.r1
AA2808470	2M0072H02
AV852307	AV852307
BG235568	na145d01.
BG231022	na143f11.
BG271430	na150f08.
W95439	ze07f06.s1
AA930101	vq58f12.r
AA191061	zq44f08.r
AI038836	Homo sapi
T74784	yc59h01.s1
A24742270	1M0290C13

C 91	14.4	40.0	80	9	AA639369	nq87e03.s	C 164	14	38.9	82	12	BH230151	BH230151	100615600
C 92	14.4	40.0	82	9	AA634670	ab26d05.r	C 165	14	38.9	87	10	BG694657	BG694657	NINSC_-1v06
C 93	14.4	40.0	84	10	T72344	yc71h07.s1	C 166	14	38.9	88	10	T63296	T63296	yc15y11.r1
C 94	14.4	40.0	84	12	A2482854	1M0308G09	C 167	14	38.9	88	12	A2339120	A2339120	1M0070P20
C 95	14.4	40.0	85	10	BG508151	smc98h05.	C 168	14	38.9	92	9	A1320353	A1320353	c3f02nm.f
C 96	14.4	40.0	86	9	AA515609	ng70a03.s	C 169	14	38.9	93	12	BH622657	BH622657	1M07090F0
C 97	14.4	40.0	87	12	A2777830	AA777830	C 170	14	38.9	93	12	BH622657	AM778403	1M07090F0
C 98	14.4	40.0	88	12	A2388906	1M0149I08	C 171	14	38.9	94	12	A2782334	A2782334	2M0022102
C 99	14.4	40.0	89	10	T73577	7f3577	C 172	14	38.9	95	10	F24664	F24664	yc44f106.s1
C 100	14.4	40.0	91	9	AA238625	mx82g02.r	C 173	14	38.9	95	10	T95120	T95120	yc44f106.s1
C 101	14.4	40.0	92	10	AA118574	mo99d11.r	C 174	14	38.9	95	10	BF507200	BF507200	3659P-10C
C 102	14.4	40.0	92	10	T72138	yc69e01.r1	C 175	14	38.9	95	12	BH230297	BH230297	1M0615780
C 103	14.4	40.0	93	10	W80226	me89f10.r1	C 176	14	38.9	96	12	A2606711	A2606711	1M0428G17
C 104	14.4	40.0	94	9	AA661504	nr18c12.s	C 177	14	38.9	97	9	AA986105	AA986105	uc81g93.x
C 105	14.4	40.0	94	9	AA159463	zo78h03.r	C 178	14	38.9	97	9	AI970541	AI970541	wf11e09.x
C 106	14.4	40.0	95	10	F35777	HSPD32788.H	C 179	14	38.9	97	9	AM342946	AM342946	f171b01.y
C 107	14.4	40.0	96	10	N30082	yw63a01.s1	C 180	14	38.9	97	10	BF156685	BF156685	f155e06.y
C 108	14.4	40.0	97	9	AA234884	zr77h01.r	C 181	14	38.9	98	9	AA087872	AA087872	mn97b09.r
C 109	14.4	40.0	98	9	AA311302	sg35b11.y	C 182	14	38.9	98	9	AM042514	AM042514	614069G10
C 110	14.4	40.0	99	10	BG217845	Be217845	C 183	14	38.9	99	9	AM14353	AM134353	f118d07.y
C 111	14.4	40.0	100	10	BF904872	IL2-MT017	C 184	13.8	38.3	36	12	BH023730	BH023730	BG01371-5
C 112	14.4	40.0	100	10	BJ060521	BJ060521	C 185	13.8	38.3	37	9	AA059414	AA059414	z195a02.r1
C 113	14.2	39.4	36	9	AL630420	AL630420	C 186	13.8	38.3	38	10	R85027	R85027	yc042c06.r
C 114	14.2	39.4	40	9	AI047706	uh82c05.r	C 187	13.8	38.3	38	10	A2809847	A2809847	2M0074102
C 115	14.2	39.4	40	10	BF970220	602273453	C 188	13.8	38.3	48	12	A2809847	B116352	602910712
C 116	14.2	39.4	50	9	AU102800	AU102800	C 189	13.8	38.3	53	12	B45081	B45081	HS-1060-BL
C 117	14.2	39.4	51	12	A2423763	1M0203E24	C 190	13.8	38.3	59	12	A2416641	A2416641	1M0192809
C 118	14.2	39.4	52	9	AA873212	oh70e06.s	C 191	13.8	38.3	64	10	R00300	R00300	yc42f04.s1
C 119	14.2	39.4	52	12	B02480	CSRL-154d4								

237	13.8	38.3	97	10	T75549	T75549 yd63h02.r1	C 310	13.4	37.2	46	12	A2452200	A2452200 1M0251K23
C 238	13.8	38.3	97	10	BF718430	BF718430 EST203.m1	311	13.4	37.2	47	12	A2838688	A2838688 2M0134B02
C 239	13.8	38.3	97	10	BF718467	BF718467 EST240.m1	312	13.4	37.2	50	9	AU102742	AU102742 AU102742
240	13.8	38.3	99	10	BF054674	BF054674 7169c01.y	C 313	13.4	37.2	50	9	AU105625	AU105625 AU105625
241	13.8	38.3	99	12	AF149659	AF149659 AF149639	C 314	13.4	37.2	50	12	A2665536	A2665536 1M0548D16
242	13.8	38.3	99	12	A2785782	A2785782 1M0030K02	C 315	13.4	37.2	51	12	A2327423	A2327423 1M0505A18
243	13.8	38.3	99	12	CNS060UL	AL415999 t7 end of	C 316	13.4	37.2	51	12	A2492896	A2492896 1M0327H14
C 244	13.8	38.3	100	9	AA453812	AA453812 aa19h03.s	C 317	13.4	37.2	52	9	AA834377	AA834377 of67e05.s
C 245	13.6	37.8	34	10	BI824749	BI824749 603033629	C 318	13.4	37.2	52	9	A1966990	A1966990 wq79a04.x
C 246	13.6	37.8	41	10	BI819153	BI819153 603036952	319	13.4	37.2	53	12	AF179999	AF179999 AF179999
C 247	13.6	37.8	42	12	A2370282	A2370282 1M0121C16	C 320	13.4	37.2	53	12	AF180000	AF180000 AF180000
C 248	13.6	37.8	51	9	AA548570	AA548570 nk50d02.s	C 321	13.4	37.2	55	12	A2341308	A2341308 1M0073D09
C 249	13.6	37.8	51	9	A1664266	A1664266 ue83e10.r	C 322	13.4	37.2	62	10	BE619792	BE619792 601473010
C 250	13.6	37.8	55	10	C21332	C21332 HUMS0000298	C 323	13.4	37.2	62	12	BH406408	BH406408 RRC1-23-4
C 251	13.6	37.8	55	12	AF107432	AF107432 AF107432	C 324	13.4	37.2	64	9	AM620188	AM620188 SMOVAPCAP
C 252	13.6	37.8	56	10	D19115	D19115 MUGS01326	C 325	13.4	37.2	66	9	AF090296	AF090296 AF090296
C 253	13.6	37.8	56	10	DA5776	DA5776 HUMGS02988	C 326	13.4	37.2	70	9	AA665485	AA665485 ag53e12.s
C 254	13.6	37.8	57	10	BE321392	BE321392 NF024D081	C 327	13.4	37.2	70	10	R19740	R19740 yg40c02.r1
C 255	13.6	37.8	58	10	AA910660	AA910660 ok65d03.s	C 328	13.4	37.2	73	9	AM507105	AM507105 ESTY00432
C 256	13.6	37.8	58	12	BE321593	BE321593 NF025D081	329	13.4	37.2	73	9	AM507161	AM507161 ESTY00498
257	13.6	37.8	58	12	A2923835	A2923835 4908.gf22	330	13.4	37.2	73	9	AM507171	AM507171 ESTY00498
258	13.6	37.8	59	10	W30055	W30055 mc26C10.r1	C 331	13.4	37.2	73	9	AM651810	AM651810 SMTD2SCAU
259	13.6	37.8	62	12	CNS02D68	AL192113 Teltraodon	C 332	13.4	37.2	75	9	A1915457	A1915457 lr28e04.x
C 260	13.6	37.8	63	9	AA460851	AA460851 zx64h10.s	C 333	13.4	37.2	76	9	A1795050	A1795050 sb75e11.y
C 261	13.6	37.8	66	12	A2495791	A2495791 1M0331B24	C 334	13.4	37.2	77	10	T711777	T711777 yc64b11.s1
C 262	13.6	37.8	67	9	AA082531	AA082531 z688c11.r	C 335	13.4	37.2	78	10	BG673171	BG673171 DRNB002
263	13.6	37.8	71	12	A2821580	A2821580 2M0094120	C 336	13.4	37.2	79	9	AA934860	AA934860 ny30f10.s
C 264	13.6	37.8	73	9	AA232349	AA232349 zr27b12.r	C 337	13.4	37.2	79	12	A2373916	A2373916 1M0126G10
C 265	13.6	37.8	73	12	A2868344	A2868344 2M0160L13	C 338	13.4	37.2	82	12	A2475784	A2475784 1M0294B07
266	13.6	37.8	75	10	BF054657	BF054657 7169a11.y	C 339	13.4	37.2	82	12	A2589955	A2589955 1M0399G18
C 267	13.6	37.8	79	9	A1873886	A1873886 wmk3d03.x	340	13.4	37.2	85	9	AA798174	AA798174 vx67h07.r
268	13.6	37.8	79	9	AA220763	AA220763 mv66f12.r	341	13.4	37.2	85	9	A1567857	A1567857 t987f09.x
C 269	13.6	37.8	79	10	H24634	H24634 y140a11.r1	342	13.4	37.2	88	9	A1951165	A1951165 w654d02.x
C 270	13.6	37.8	79	12	A2813967	A2813967 2M0081N13	343	13.4	37.2	88	10	N83319	N83319 EC0185F.Hum
271	13.6	37.8	82	9	AA014982	AA014982 mh28b03.r	344	13.4	37.2	89	10	BF166160	BF166160 601776812
C 272	13.6	37.8	85	9	AA168898	AA168898 ms39a06.r	C 345	13.4	37.2	89	12	A2330728	A2330728 1M0056B10
C 273	13.6	37.8	86	12	A0797276	A0797276 RPCI-22-2	346	13.4	37.2	89	12	A2369147	A2369147 1M0119003
274	13.6	37.8	87	9	A1874091	A1874091 wmk4e07.x	C 347	13.4	37.2	91	9	A1048394	A1048394 uh54h03.r
C 275	13.6	37.8	87	9	AA276636	AA276636 vc45b07.r	C 348	13.4	37.2	91	10	C011740	C011740 HUMGS000361
C 276	13.6	37.8	87	9	AA475168	AA475168 v995f04.r	C 349	13.4	37.2	92	9	AA075935	AA075935 zm76f11.r
277	13.6	37.8	88	9	AA888085	AA888085 nq98h07.s	C 350	13.4	37.2	92	12	CNS02D05	AL214322 AJ396661
278	13.6	37.8	88	9	AA991534	AA991534 os59f02.s	C 351	13.4	37.2	93	9	AJ396661	AJ396661 AJ396661
C 279	13.6	37.8	88	9	A1384188	A1384188 fbl17f08.y	C 352	13.4	37.2	94	9	AV833328	AV833328 AV833328
C 280	13.6	37.8	88	12	A2596718	A2596718 1M0410H12	C 353	13.4	37.2	94	12	A29733567	A29733567 2M0247P17
C 281	13.6	37.8	90	9	AA267664	AA267664 mc29c12.r	354	13.4	37.2	95	9	AA693521	AA693521 ah33f07.s
282	13.6	37.8	90	10	BG409284	BG409284 gp90a06.y	355	13.4	37.2	96	10	H52029	H52029 y044e07.r1
283	13.6	37.8	90	10	BG409310	BG409310 gp90a12.y	356	13.4	37.2	97	10	BG812139	BG812139 da1f66a10.
284	13.6	37.8	90	12	A2579572	A2579572 1M0367M04	C 357	13.4	37.2	97	10	H68060	H68060 yr74h04.r1
285	13.6	37.8	90	12	A2767516	A2767516 1M0566C17	C 358	13.4	37.2	98	10	BG405761	BG405761 sac37f07.
286	13.6	37.8	91	9	AA914944	AA914944 vz10c05.r	C 359	13.4	37.2	98	9	A1607774	A1607774 uh58a06.x
287	13.6	37.8	91	9	A1571584	A1571584 lr68a02.x	C 360	13.4	37.2	100	9	A1719091	A1719091 as65907.x
C 288	13.6	37.8	92	10	H27916	H27916 y074e07.s1	361	13.4	37.2	100	10	BG994742	BG994742 PML-HT100
C 289	13.6	37.8	92	10	R94079	R94079 yr74e07.s1	C 362	13.4	37.2	100	10	BG994742	BG994742 PML-HT100
290	13.6	37.8	93	10	BF057945	BF057945 7165e10.y	C 363	13.4	37.2	100	10	BI048752	BI048752 PM2-PM002
291	13.6	37.8	94	9	AA909443	AA909443 o114d01.s	C 364	13.4	37.2	100	10	BI398555	BI398555 952002G07
292	13.6	37.8	94	9	A1453717	A1453717 t139d08.x	365	13.2	36.7	30	10	R16642	R16642 yf43h06.r1
293	13.6	37.8	94	10	R28917	R28917 F1-29D.22.w	366	13.2	36.7	43	9	A1790425	A1790425 u010a08.x
C 294	13.6	37.8	95	9	A1299931	A1299931 qm559b03.x	367	13.2	36.7	45	10	BE911608	BE911608 601663085
295	13.6	37.8	95	12	BH614570	BH614570 258D9.Su	C 368	13.2	36.7	47	12	A2826169	A2826169 2M0101D16
296	13.6	37.8	98	10	BJ058978	BJ058978 BJ058978	369	13.2	36.7	49	9	AA993146	AA993146 ot77a10.s
C 297	13.6	37.8	98	10	R19790	R19790 yg28f10.r1	370	13.2	36.7	49	9	A1623465	A1623465 ts19a05.x
298	13.6	37.8	98	12	A2375618	A2375618 1M0129P03	C 371	13.2	36.7	50	9	AU104961	AU104961 AU104961
299	13.6	37.8	98	12	A2812508	A2812508 2M0079A15	C 372	13.2	36.7	50	10	BG212917	BG212917 na156a06.
C 300	13.6	37.8	99	10	BG31431	BG31431 na142d03.	373	13.2	36.7	52	9	A1203654	A1203654 qf48a05.x
301	13.6	37.8	99	10	X93840	X93840 HSIIMB159.H	C 374	13.2	36.7	52	9	AM695399	AM695399 NF094C075
C 302	13.6	37.8	100	9	AA015156	AA015156 m163a07.r	375	13.2	36.7	53	10	BG211727	BG211727 na152g11.
303	13.6	37.8	100	10	BG264854	BG264854 947023D07	376	13.2	36.7	53	12	TA252D05Q	TA252D05Q T.brucel
304	13.6	37.8	100	10	BG993529	BG993529 PM0-HT091	377	13.2	36.7	56	10	BG2171341	BG2171341 na149c02.
305	13.6	37.8	100	10	R37055	R37055 yf54a03.s1	C 378	13.2	36.7	58	9	A1265422	A1265422 u010e07.x
306	13.6	37.8	100	12	TA288D03P	TA288D03P T.brucel	C 379	13.2	36.7	63	10	BG2171540	BG2171540 na158g04.
C 307	13.4	37.2	28	12	A2642724	A2642724 1M0505G19	380	13.2	36.7	63	10	BG2172246	BG2172246 na133a10.
C 308	13.4	37.2	37	9	A1032109	A1032109 ot57a01.s	381	13.2	36.7	64	9	A1663959	A1663959 u116f02.r
C 309	13.4	37.2	43	9	A1335574	A1335574 qt30g11.x	382	13.2	36.7	64	10	BG370387	BG370387 na131f10.

C 383	13.2	36.7	64	10	BM434808	1RT14C11	456	13	36.1	48	10	BI085472	BI085472	602869964
C 384	13.2	36.7	64	12	TA69E07P	Brucei	457	13	36.1	49	9	AA813812	AA813812	a172c08.s
C 385	13.2	36.7	67	10	BG370450	na133q07	C 458	13	36.1	50	12	A2781441	A2781441	2M0019N14
C 386	13.2	36.7	68	10	BG271399	na150b05	C 459	13	36.1	51	10	BF583696	BF583696	602096712
C 387	13.2	36.7	68	10	BG271739	na153a11	C 460	13	36.1	51	12	A2777345	A2777345	2M0011M10
C 388	13.2	36.7	68	10	BG271766	na153a10	C 461	13	36.1	52	9	AM692147	AM692147	NF048B04S
C 389	13.2	36.7	69	10	BG272596	na128c07	C 462	13	36.1	52	10	BI692727	BI692727	603343394
C 390	13.2	36.7	69	9	AU013374	AU013374	C 463	13	36.1	52	12	A2596774	A2596774	1M0410D16
C 391	13.2	36.7	69	9	AU013456	AU013456	C 464	13	36.1	54	12	A2636428	A2636428	1M0495616
C 392	13.2	36.7	69	9	AU013458	AU013458	C 465	13	36.1	55	9	AA863404	AA863404	oh42f05.s
C 393	13.2	36.7	70	10	W75405	me52g11.r1	C 466	13	36.1	55	9	AA923752	AA923752	cm39f05.s
C 394	13.2	36.7	72	12	AA412871	AA412871	C 467	13	36.1	55	12	A2332169	A2332169	1M0060R06
C 395	13.2	36.7	72	12	FR0011666	FR0011666	C 468	13	36.1	55	12	A2433298	A2433298	1M0021P04
C 396	13.2	36.7	74	10	T80053	Yd22604..s1	C 469	13	36.1	56	12	A2959219	A2959219	2M0226L15
C 397	13.2	36.7	75	9	AA038845	ml94b11.r	C 470	13	36.1	58	9	AA912277	AA912277	0195B06.s
C 398	13.2	36.7	77	9	AA580890	nc81903.r	C 471	13	36.1	60	12	A2810984	A2810984	2M0076H23
C 399	13.2	36.7	78	12	CNS03K9R	Al247896	C 472	13	36.1	62	10	F29764	F29764	HSPD19838
C 400	13.2	36.7	78	12	TR207G090	Al475880	C 473	13	36.1	62	12	A2493333	A2493333	1M0327022
C 401	13.2	36.7	80	12	AO917592	DI1BCM141	C 474	13	36.1	63	9	AA995928	AA995928	cu93h03.s
C 402	13.2	36.7	80	12	CNS01VRQ	Al169487	C 475	13	36.1	63	9	AA072607	AA072607	mm74a08.r
C 403	13.2	36.7	81	10	BJ063899	BJ063899	C 476	13	36.1	64	9	AI807861	AI807861	wf43e03.x
C 404	13.2	36.7	81	12	A2799436	2M0056J22	C 477	13	36.1	64	10	BF400386	BF400386	SMOVC3MCM
C 405	13.2	36.7	82	9	AA707036	z132C06.s	C 478	13	36.1	65	10	F29764	F29764	HSPD19838
C 406	13.2	36.7	82	9	AA282522	ZS90F03.s	C 479	13	36.1	66	9	AA265581	AA265581	mu66h06.r
C 407	13.2	36.7	82	10	T272220	MTO-208	C 480	13	36.1	66	12	A2509413	A2509413	1M0352B21
C 408	13.2	36.7	83	9	AA853178	NHRCae03	C 481	13	36.1	66	12	A2658120	A2658120	1M0534P10
C 409	13.2	36.7	83	12	A2774496	2M0004G02	C 482	13	36.1	69	12	HSMC01C05	HSMC01C05	h.sapiens D
C 410	13.2	36.7	84	12	A2628284	1M0480K17	C 483	13	36.1	70	9	AI267761	AI267761	ap64b06.x
C 411	13.2	36.7	85	10	B1547093	603190K29	C 484	13	36.1	70	9	AA545052	AA545052	v170h12.r
C 412	13.2	36.7	87	10	T61060	YD57F12..r1	C 485	13	36.1	70	12	HSMC6B05	HSMC6B05	h.sapiens D
C 413	13.2	36.7	88	9	AM058325	wx19a05.x	C 486	13	36.1	71	12	A2780697	A2780697	2M0018G04
C 414	13.2	36.7	88	9	AA600757	np44C02.s	C 487	13	36.1	72	9	AA394054	AA394054	z136a07.r
C 415	13.2	36.7	89	9	AI586282	vr92d11.x	C 488	13	36.1	72	10	BI649061	BI649061	603277244
C 416	13.2	36.7	89	10	BM041565	603614Z87	C 489	13	36.1	72	12	A2792344	A2792344	2M0043C15
C 417	13.2	36.7	89	12	A2610456	1M0435D18	C 490	13	36.1	73	9	AA895520	AA895520	vx51b03.r
C 418	13.2	36.7	89	12	BH227116	1006137C0	C 491	13	36.1	73	9	AI046706	AI046706	uh54b03.r
C 419	13.2	36.7	90	9	AA097596	mm85g05.r	C 492	13	36.1	73	9	AI334986	AI334986	tb21d02.x
C 420	13.2	36.7	90	9	AL047504	DF2P586A	C 493	13	36.1	73	10	BI747072	BI747072	rm35e09.y
C 421	13.2	36.7	91	9	AA857283	Oh96d05.s	C 494	13	36.1	74	9	AI274464	AI274464	qv61b05.x
C 422	13.2	36.7	92	10	BM042811	603616222	C 495	13	36.1	74	9	AA509888	AA509888	vh51d12.r
C 423	13.2	36.7	92	10	R62490	Y157F12..r1	C 496	13	36.1	74	10	BI108066	BI108066	602902456
C 424	13.2	36.7	93	9	AA159462	z078h01.r	C 497	13	36.1	74	10	W74829	W74829	me42g09..r1
C 425	13.2	36.7	94	9	AI558590	fb68a05.y	C 498	13	36.1	74	12	A2479612	A2479612	1M0300G21
C 426	13.2	36.7	94	9	AA444519	ve74g10.r	C 499	13	36.1	74	12	A2810600	A2810600	2M0076B16
C 427	13.2	36.7	94	10	BG153023	BG153023	C 500	13	36.1	75	12	A2584287	A2584287	1M0388N08
C 428	13.2	36.7	94	10	H55457	CHR220396.C	C 501	13	36.1	77	9	AI988585	AI988585	sd04f08.y
C 429	13.2	36.7	94	12	A2433675	1M0219110	C 502	13	36.1	77	10	BF447360	BF447360	nae41h01
C 430	13.2	36.7	94	12	A2783134	A2783134	C 503	13	36.1	77	12	CNS02YU9	CNS02YU9	h.sapiens D
C 431	13.2	36.7	95	9	AA705353	z189e03.s	C 504	13	36.1	78	9	AM169677	AM169677	x130g06.x
C 432	13.2	36.7	95	10	T80645	Yd92f03..s1	C 505	13	36.1	80	10	H26218	H26218	y153e02..r1
C 433	13.2	36.7	96	12	CNS01YLV	Al173164	C 506	13	36.1	81	9	AA813818	AA813818	a172d03.s
C 434	13.2	36.7	97	9	AA011784	mg92b08.r	C 507	13	36.1	81	10	BI247002	BI247002	602960316
C 435	13.2	36.7	97	9	AI699715	z121a11.x	C 508	13	36.1	81	10	BE310690	BE310690	601089610
C 436	13.2	36.7	97	9	AA623870	vg73g08.s	C 509	13	36.1	82	12	HSMC03D03	HSMC03D03	h.sapiens D
C 437	13.2	36.7	97	10	BM283575	k149c04.y	C 510	13	36.1	83	9	AA744552	AA744552	ny79c12.s
C 438	13.2	36.7	98	10	BG088058	nan20a10	C 511	13	36.1	83	12	A2800638	A2800638	2M0038F17
C 439	13.2	36.7	98	10	H74532	623 Random	C 512	13	36.1	83	12	TA257A040	TA257A040	q176d02..r
C 440	13.2	36.7	99	9	AM368196	CMO-HT017	C 513	13	36.1	85	9	AA762642	AA762642	vg61h09.r
C 441	13.2	36.7	99	10	BG290992	602386983	C 514	13	36.1	85	9	AI081847	AI081847	ov24b02.x
C 442	13.2	36.7	100	9	AA566732	2F-A116.z	C 515	13	36.1	85	9	AI130915	AI130915	t476a01.x
C 443	13.2	36.7	100	10	BE399543	WHE0037.F	C 516	13	36.1	85	9	AA257813	AA257813	MB12S3JH1
C 444	13.2	36.7	100	12	AF088169	AF088169	C 517	13	36.1	85	9	BE139668	BE139668	xt71a11.x
C 445	13.2	36.7	100	12	BH614993	KG03863-3	C 518	13	36.1	85	9	AA585374	AA585374	TH193 HTC
C 446	13.2	36.7	100	12	A2395654	1M0159G20	C 519	13	36.1	86	10	R131943	R131943	vh62e12..s1
C 447	13.2	36.7	100	12	A2616956	1M0448B06	C 520	13	36.1	87	9	AI478728	AI478728	tm01h03.x
C 448	13.2	36.7	100	12	A2875526	2M0189M09	C 521	13	36.1	88	10	H25273	H25273	y145f10..s1
C 449	13.2	36.7	100	12	AI377772	te62b10..x	C 522	13	36.1	88	10	NA8035	NA8035	yz23g02..r1
C 450	13.2	36.7	100	12	AA465345	1M0275007	C 523	13	36.1	89	10	BF506950	BF506950	11349P-17
C 451	13.2	36.7	100	12	AA133553	zoi14b11.r	C 524	13	36.1	90	10	AI1904511	AI1904511	PM-BT057-
C 452	13.2	36.7	100	12	TA188F11P	AI4783C02.T	C 525	13	36.1	90	10	H27542	H27542	y161C03..s1
C 453	13.2	36.7	100	12	A2324505	1M0046B02	C 526	13	36.1	91	9	AI001782	AI001782	ot41g03.s
C 454	13.2	36.7	100	12	A2785693	2M0029P15	C 527	13	36.1	91	9	AI559146	AI559146	tg42a11.x
C 455	13.2	36.7	100	12	B0052697	B0052697	C 528	13	36.1	91	12	A2324964	A2324964	1M0047G04

529	13	36.1	93	10	BM320187	BM320187 rs86c07.y	C 602	12.8	35.6	73	10	D18646	D18646 MUSGS01707
530	13	36.1	94	9	AA916621	AA916621 oh83h11.s	C 603	12.8	35.6	73	12	CNS014FO	AL071647 retradon
531	13	36.1	94	10	BM310585	BM310585 i950a02.x	C 604	12.8	35.6	74	9	AA207453	AA207453 mw87c02.r
532	13	36.1	94	10	BF507107	BF507107 19188P-19	C 605	12.8	35.6	74	10	BG022663	BG022663 daa78h08.
533	13	36.1	94	12	A2922137	A2922137 MACoC1D06	C 606	12.8	35.6	75	10	BF385911	BF385911 602046079
534	13	36.1	95	9	AM458210	AM458210 sh79g10.y	C 607	12.8	35.6	77	10	BI455970	BI455970 603170413
535	13	36.1	95	9	AM630585	AM630585 hh81g04.y	C 608	12.8	35.6	77	10	W20616	W20616 mb90g12.r1
536	13	36.1	95	10	BF787752	BF787752 602113508	C 609	12.8	35.6	77	10	BF461613	BF461613 ui-M-CG0P
537	13	36.1	95	10	BG151355	BG151355 na136g03	C 610	12.8	35.6	77	12	A2816336	A2816336 2M0085G02
538	13	36.1	95	10	BG256984	BG256984 602370487	C 611	12.8	35.6	78	9	A1798246	A1798246 t322b01.x
539	13	36.1	96	10	BE636908	BE636908 WHE1805-1	C 612	12.8	35.6	78	10	BF188658	BF188658 601775572
540	13	36.1	97	9	A1322965	A1322965 ma37a04.y	C 613	12.8	35.6	79	9	A1882978	A1882978 fc45a01.x
541	13	36.1	97	10	BG151773	BG151773 na664c08.	C 614	12.8	35.6	79	10	BE287727	BE287727 601095007
542	13	36.1	98	9	AA440393	AA440393 AVA40393.r	C 615	12.8	35.6	80	9	A1933809	A1933809 wp92f01.x
543	13	36.1	98	9	AA443529	AA443529 zw33907.r	C 616	12.8	35.6	80	10	BI081792	BI081792 602879692
544	13	36.1	98	12	AA464105	AA464105 zx86e05.r	C 617	12.8	35.6	80	10	D12397	D12397 HUM00TW118
545	13	36.1	98	12	A2639208	A2639208 IM0499102	C 618	12.8	35.6	80	12	A2634856	A2634856 IM0490G19
546	13	36.1	98	12	BH224673	BH224673 1006120E0	C 619	12.8	35.6	80	12	A2759343	A2759343 IM0551J24
547	13	36.1	98	12	TA154E03Q	TA154E03Q T. bruce1	C 620	12.8	35.6	81	9	AM189692	AM189692 xk93d08.x
548	13	36.1	99	10	BE652177	BE652177 ui-M-ANO-	C 621	12.8	35.6	81	10	BG065539	BG065539 H3033C11-
549	13	36.1	100	9	AM842018	AM842018 RCO-CND02	C 622	12.8	35.6	81	12	BH231170	BH231170 1006160G0
550	13	36.1	100	9	BE130029	BE130029 94503C01	C 623	12.8	35.6	82	9	A1621003	A1621003 tu87g04.x
551	13	36.1	100	10	BI021861	BI021861 RCS-MT025	C 624	12.8	35.6	82	9	A1957106	A1957106 ui75d03.x
552	13	36.1	100	10	BI448290	BI448290 dae71a10.	C 625	12.8	35.6	82	10	F31564	F31564 HSPD22856.H
553	13	36.1	100	10	BE770198	BE770198 PM4-FT005	C 626	12.8	35.6	82	10	BE978366	BE978366 bs677609.y
554	13	36.1	100	10	BF362465	BF362465 OV2-NN005	C 627	12.8	35.6	82	12	A2795408	A2795408 2M0049E07
555	13	36.1	100	12	A2592212	A2592212 IM0402023	C 628	12.8	35.6	83	10	BG938692	BG938692 cn27g07.y
556	12.8	35.6	100	12	A2400041	A2400041 IM0166H12	C 629	12.8	35.6	85	9	A1683623	A1683623 tw52g11.x
557	12.8	35.6	41	9	AA846329	AA846329 aj35c10.s	C 630	12.8	35.6	85	9	AA271975	AA271975 vb79d07.r
558	12.8	35.6	41	12	A2399407	A2399407 IM0165D15	C 631	12.8	35.6	86	9	AA585223	AA585223 KTH113.HT
559	12.8	35.6	42	9	AV673240	AV673240 AVF73240	C 632	12.8	35.6	87	10	BI694143	BI694143 603342661
560	12.8	35.6	42	12	A2303641	A2303641 IM0003K07	C 633	12.8	35.6	88	9	AA912340	AA912340 ol97g06.s
561	12.8	35.6	43	9	A1538940	A1538940 tp75c09.x	C 634	12.8	35.6	88	9	A1243784	A1243784 que6a07.x
562	12.8	35.6	43	10	BG866682	BG866682 602785673	C 635	12.8	35.6	88	10	BF781247	BF781247 602106919
563	12.8	35.6	44	10	H64101	H64101 yr57e01.r1	C 636	12.8	35.6	88	10	D38700	D38700 HUMC1402.Hu
564	12.8	35.6	46	9	AA936139	AA936139 om57f07.s	C 637	12.8	35.6	89	10	N84695	N84695 J0519F.Huma
565	12.8	35.6	46	9	A1033006	A1033006 ox22e05.s	C 638	12.8	35.6	90	9	AA003377	AA003377 mg49a08.r
566	12.8	35.6	46	9	A1940962	A1940962 sb82b02.y	C 639	12.8	35.6	90	12	A2766732	A2766732 IM0564E04
567	12.8	35.6	47	10	BF139695	BF139695 601785340	C 640	12.8	35.6	91	9	A1318169	A1318169 ta73g09.x
568	12.8	35.6	48	10	BM394294	BM394294 50072-2-3	C 641	12.8	35.6	91	9	AA208150	AA208150 mw90f12.r
569	12.8	35.6	48	12	A2317194	A2317194 IM0035112	C 642	12.8	35.6	91	9	AA257032	AA257032 zp48a05.r
570	12.8	35.6	49	12	A2656928	A2656928 IM0532115	C 643	12.8	35.6	91	9	AA414841	AA414841 vc70d03.s
571	12.8	35.6	50	9	AU104380	AU104380 AU104380	C 644	12.8	35.6	91	10	W43928	W43928 mc73e08.r1
572	12.8	35.6	51	9	A1105625	A1105625 M-EST204	C 645	12.8	35.6	91	12	BH233121	BH233121 1006171G0
573	12.8	35.6	51	12	A2867661	A2867661 2M0178005	C 646	12.8	35.6	92	10	BG272239	BG272239 nah31h07.
574	12.8	35.6	52	9	AA427233	AA427233 veb3e12.r	C 647	12.8	35.6	92	10	BG578578	BG578578 d8c35b05.
575	12.8	35.6	52	12	A2311262	A2311262 IM0026B12	C 648	12.8	35.6	93	10	Z25780	Z25780 pha289u71D0
576	12.8	35.6	53	12	A2826318	A2826318 2M0101O22	C 649	12.8	35.6	93	12	A2619345	A2619345 IM0451P16
577	12.8	35.6	55	10	BG271403	BG271403 na150b10.	C 650	12.8	35.6	94	9	AA066027	AA066027 m154b03.r
578	12.8	35.6	55	12	A2595220	A2595220 IM0407N07	C 651	12.8	35.6	94	9	A1397420	A1397420 fb22a11.y
579	12.8	35.6	55	12	B00786	B00786 CSRL-11C3-U	C 652	12.8	35.6	94	9	AA398636	AA398636 zt74f03.s
580	12.8	35.6	57	10	N30936	N30936 yx50e08.r1	C 653	12.8	35.6	94	10	BG498730	BG498730 602544353
581	12.8	35.6	58	12	A2780547	A2780547 2M0018D03	C 654	12.8	35.6	94	10	BM307778	BM307778 s8k33h02.
582	12.8	35.6	59	12	A2596649	A2596649 IM0410J02	C 655	12.8	35.6	94	12	BH233352	BH233352 1006174D0
583	12.8	35.6	60	10	BG231459	BG231459 na142h07.	C 656	12.8	35.6	95	9	AA092306	AA092306 116554.se
584	12.8	35.6	62	9	AA852727	AA852727 NHTBCae15	C 657	12.8	35.6	96	9	AA105914	AA105914 m182a11.r
585	12.8	35.6	62	10	BF383963	BF383963 602045386	C 658	12.8	35.6	96	9	A1623636	A1623636 ts22c09.x
586	12.8	35.6	63	9	AA486663	AA486663 ab16d10.r	C 659	12.8	35.6	96	10	BI850097	BI850097 lma9eC01
587	12.8	35.6	64	9	A1570111	A1570111 tr74d11.x	C 660	12.8	35.6	96	12	A2603298	A2603298 IM0422H01
588	12.8	35.6	65	10	BG370292	BG370292 na129g12.	C 661	12.8	35.6	97	12	BH225322	BH225322 1006125F0
589	12.8	35.6	65	10	BI687371	BI687371 603313585	C 662	12.8	35.6	97	9	A1224438	A1224438 gw99g01.x
590	12.8	35.6	65	12	BH226595	BH226595 1006133C0	C 663	12.8	35.6	97	10	A1819670	A1819670 w159g05.x
591	12.8	35.6	66	12	A2500986	A2500986 IM00339F08	C 664	12.8	35.6	97	10	BG058068	BG058068 nah20b08.
592	12.8	35.6	67	9	AA986998	AA986998 uc81a09.y	C 665	12.8	35.6	97	10	BG099268	BG099268 mb99d03.
593	12.8	35.6	68	10	BF476509	BF476509 naa27b04.	C 666	12.8	35.6	97	10	H25644	H25644 y150g07.r1
594	12.8	35.6	68	12	A2662900	A2662900 IM0342F13	C 667	12.8	35.6	98	9	AA789016	AA789016 ah32b09.s
595	12.8	35.6	70	12	TA435H09Q	TA435H09Q T. bruce1	C 668	12.8	35.6	98	10	AA153155	AA153155 mrl4a03.r
596	12.8	35.6	70	12	AF107425	AF107425 v161d12.s	C 669	12.8	35.6	98	10	BG223002	BG223002 nah41c12.
597	12.8	35.6	71	12	B39607	B39607 HS-1050-A1-	C 670	12.8	35.6	98	10	T83623	T83623 yd64f02.r1
598	12.8	35.6	71	12	BI520673	BI520673 603071655	C 671	12.8	35.6	98	12	A2316421	A2316421 IM0034K04
599	12.8	35.6	72	12	TA116A05P	TA116A05P T. bruce1	C 672	12.8	35.6	98	12	A2864812	A2864812 2M0174A07
600	12.8	35.6	72	12	TA116A05P	TA116A05P T. bruce1	C 673	12.8	35.6	99	9	AA807995	AA807995 nu98h12.s
601	12.8	35.6	73	9	A1875776	A1875776 uj21f11.x	C 674	12.8	35.6	99	9	A1561657	A1561657 vvo2g06.x

675	12.8	35.6	99	10	BG151484	BG151484 na138c03.	748	12.6	35.0	75	12	A2399801	A2399801 1M0165L17
676	12.8	35.6	99	10	B1094731	B1094731 Est-CD34N	749	12.6	35.0	76	10	A1560471	A1560471 tnl1c08.x
677	12.8	35.6	100	9	AL644907	AL644907 AL644907	750	12.6	35.0	76	10	BG059366	BG059366 nah50d01.
678	12.8	35.6	100	9	AA292564	AA292564 zt31a06.r	751	12.6	35.0	76	10	BG109745	BG109745 602280882
679	12.8	35.6	100	10	BF757141	BF757141 MRO-Cr045	752	12.6	35.0	76	10	BG271719	BG271719 na152f10.
680	12.8	35.6	100	10	B1060570	B1060570 MR4-UT005	753	12.6	35.0	76	12	A2839194	A2839194 2M0135P07
681	12.8	35.6	100	10	A2596265	A2596265 1M0409K22	754	12.6	35.0	77	10	BG1970479	A1970479 wq3d03.x
682	12.6	35.0	28	10	W19872	W19872 2b40f108.r1	755	12.6	35.0	77	10	BG271490	BG271490 na157h03.x
683	12.6	35.0	31	12	A1142775	A1142775 qa26a02.s	756	12.6	35.0	78	12	A2774980	A2774980 2M0004D19
684	12.6	35.0	33	12	FA210G070	FA210G070 T. brucei	757	12.6	35.0	78	12	BH217936	BH217936 1006062D0
685	12.6	35.0	40	9	A1268767	A1268767 q048c06.x	758	12.6	35.0	79	9	A1001910	A1001910 ct42c12.s
686	12.6	35.0	42	12	A2771500	A2771500 1M0573M12	759	12.6	35.0	79	9	A4401568	A4401568 zu62a08.r
687	12.6	35.0	43	10	H45703	H45703 yp23g05.s1	760	12.6	35.0	79	12	A2404153	A2404153 1M0172L16
688	12.6	35.0	45	10	Bj028703	Bj028703 B1028703	761	12.6	35.0	79	12	A2575975	A2575975 AsT-T31D0
689	12.6	35.0	45	10	BE336369	BE336369 601086943	762	12.6	35.0	80	12	CNS02R5U	A210171 Tetracodon
690	12.6	35.0	46	9	AA238784	AA238784 mx82h02.r	763	12.6	35.0	80	12	TA16001P	A1451509 T. brucei
691	12.6	35.0	46	12	A2800704	A2800704 2M0058D22	764	12.6	35.0	81	10	BG063406	BG063406 H3006H07-
692	12.6	35.0	47	10	H99103	H99103 yx18h05.s1	765	12.6	35.0	82	9	A1959186	A1959186 fd07h08.y
693	12.6	35.0	49	10	BG489537	BG489537 602517943	766	12.6	35.0	82	9	AA537780	AA537780 vj33g04.r
694	12.6	35.0	50	9	AU103184	AU103184 AU103184	767	12.6	35.0	82	9	BM052859	BM052859 1e67c03.y
695	12.6	35.0	50	9	AU103247	AU103247 AU103247	768	12.6	35.0	82	12	TA80D10P	A461433 T. brucei
696	12.6	35.0	50	9	AU103248	AU103248 AU103248	769	12.6	35.0	83	9	AA832007	AA832007 oc97d09.s
697	12.6	35.0	50	9	AU103996	AU103996 AU103996	770	12.6	35.0	83	9	AA426735	AA426735 vfi8a04.s
698	12.6	35.0	50	9	AU104780	AU104780 AU104780	771	12.6	35.0	83	10	C20833	C20833 HUMGS000488
699	12.6	35.0	50	9	AU104880	AU104880 AU104880	772	12.6	35.0	84	9	AA152834	AA152834 z128c12.r
700	12.6	35.0	50	9	AU106463	AU106463 AU106463	773	12.6	35.0	84	12	BE222274	BE222274 7p50d01.x
701	12.6	35.0	50	12	A0073798	A0073798 EP(3)3181	774	12.6	35.0	84	12	A2587706	A2587706 1M0395L01
702	12.6	35.0	51	9	AA286026	AA286026 vc34c04.r	775	12.6	35.0	84	12	BH232655	BH232655 1006168H0
703	12.6	35.0	54	10	BG272667	BG272667 nah35c05.	776	12.6	35.0	85	9	A1955380	A1955380 wli0g03.x
704	12.6	35.0	55	9	AA808845	AA808845 nv21c09.r	777	12.6	35.0	85	12	CNS03LOT	A1249734 Tetracodon
705	12.6	35.0	55	9	A1154891	A1154891 ud82d11.r	778	12.6	35.0	86	9	AM638801	AM638801 D174g02.w
706	12.6	35.0	55	9	A1507679	A1507679 sb10c04.y	779	12.6	35.0	86	12	A2589559	A2589559 1M0398D08
707	12.6	35.0	55	10	U17539	U17539 HSU17539 Hu	780	12.6	35.0	87	10	BU059232	BU059232 BJO59232
708	12.6	35.0	56	12	A2641076	A2641076 ah26b04.s	781	12.6	35.0	87	10	BF056768	BF056768 7k08h12.x
709	12.6	35.0	58	9	AA706604	AA706604 vb60h03.r	782	12.6	35.0	87	12	FR0013972	A1005216 F. rubripes
710	12.6	35.0	58	9	AA272161	AA272161 yc83e02.r1	783	12.6	35.0	88	9	A1193977	A1193977 ge81b03.x
711	12.6	35.0	58	10	T74212	T74212 ycs83e02.r1	784	12.6	35.0	88	9	A1356331	A1356331 qz26a02.x
712	12.6	35.0	59	12	A2423198	A2423198 1M0202M08	785	12.6	35.0	88	9	A1356331	A1356331 qz26a02.x
713	12.6	35.0	59	12	B00011	B00011 CSR1-100b8-	786	12.6	35.0	88	9	A1721224	A1721224 as68c05.x
714	12.6	35.0	60	12	A2594010	A2594010 1M0405C21	787	12.6	35.0	88	9	A1906820	A1906820 IL-BT126-
715	12.6	35.0	60	12	A2633250	A2633250 1M0488E24	788	12.6	35.0	88	10	B1768376	B1768376 603053683
716	12.6	35.0	63	10	BG271913	BG271913 na160b10.	789	12.6	35.0	88	10	W79792	W79792 z473a09.r1
717	12.6	35.0	63	10	BG272058	BG272058 na162c06.	790	12.6	35.0	89	9	AA174828	AA174828 ms81f06.r
718	12.6	35.0	63	10	BE738562	BE738562 601572843	791	12.6	35.0	89	9	AA485016	AA485016 aa39f08.r
719	12.6	35.0	64	9	A1530122	A1530122 u189d07.y	792	12.6	35.0	89	12	A2310711	A2310711 1M0025K13
720	12.6	35.0	64	9	AA292260	AA292260 zt51h07.s	793	12.6	35.0	89	12	A2441956	A2441956 1M0234I20
721	12.6	35.0	64	12	B1097415	B1097415 SMOV3MCM	794	12.6	35.0	89	12	A2758176	A2758176 1M0550M02
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723	12.6	35.0	65	10	BF301324	BF301324 602029770	796	12.6	35.0	89	12	A2797146	A2797146 2M0053M11
724	12.6	35.0	65	12	A2846737	A2846737 2M0147L05	797	12.6	35.0	89	12	B42227	B42227 HS-1055-B1-
725	12.6	35.0	67	9	AA930803	AA930803 my55b03.r	798	12.6	35.0	90	9	AA065613	AA065613 mm08h11.r
726	12.6	35.0	67	9	AA984247	AA984247 am83a04.s	799	12.6	35.0	90	9	AA199989	AA199989 mu08d07.r
727	12.6	35.0	67	10	W14885	W14885 mb29f03.r1	800	12.6	35.0	90	12	A2427865	A2427865 1M0210C07
728	12.6	35.0	67	12	BH215664	BH215664 1006028A1	801	12.6	35.0	91	9	AA993677	AA993677 ct97a10.s
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C 862	12.4	34.4	52	12	A2519105	A2519105 1006013H1	935	12.4	34.4	85	12	A2653600	A2653600 1M0468M22
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870	12.4	34.4	59	12	BH416465	BH416465 1007048C0	943	12.4	34.4	88	10	BG059580	BG059580 naf42c06.
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## ALIGNMENTS

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DEFINITION 601330055F1 NCI_CGAP_Mam6 Mus musculus CDNA clone IMAGE:3707725 5',
mRNA sequence.
ACCESSION BE571706
VERSION BE571706.1 GI:9815426
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS 1 (bases 1 to 61)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM8925 row: n column: 14
High quality sequence stop: 61.
Location/Qualifiers
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## FEATURES

## Source

1..61

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/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPOrt6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Investigator
providing samples: Jeffrey Green, M.D., NIH"
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## BASE COUNT

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28 a
15 c
9 g
9 t
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Query Match 48.9%; Score 17.6; DB 10; Length 61;
Best Local Similarity 71.9%; Pred. No. 6.3e+03;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Qy 4 aaagcttcacatagccagcaccaagt 35
Db 20 ATACCTCACACCATGATCCGACATACAGT 51
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similar to TR:G1220358 G1220358 RNA POLYMERASE II. ;, mRNA
sequence.
ACCESSION AA256029
VERSION AA256029.1 GI:1891569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 64)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert length: 619 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
```

## FEATURES

## Source

1..64

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:686521"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+ IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGACAGCGAGCGCGCCCTCATTTTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

## BASE COUNT

```
23 a
16 c
11 g
14 t
```



Query Match	48.3%	Score 17.6	DB 9	Length 64
Best Local Similarity	83.3%	Pred. No. 6.4e+03		
Matches 20	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Qy	12	caccatgagccagcaccacaagt 35		
Db	13	CACCATTTACAAGGACACCAAGT 36		
RESULT 3				
LOCUS	TA386B040/c	70 bp	DNA	linear GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 386B04, reverse sequence,			
ACCESSION	AL498260			
VERSION	AL498260.1			
KEYWORDS	GSS.			
SOURCE	Trypanosoma brucei.			
ORGANISM	Trypanosoma brucei.			
REFERENCE	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.			
AUTHORS	1 (bases 1 to 70) Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk			
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: neisayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at <a href="http://www.sanger.ac.uk/projects/T-brucei/">http://www.sanger.ac.uk/projects/T-brucei/</a> .			
FEATURES	Location/Qualifiers			
source	1..70 /organism="Trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="386B04"			
BASE COUNT	20 a 13 c 11 g 26 t			
ORIGIN				
Query Match	48.3%	Score 17.4	DB 12	Length 70
Best Local Similarity	77.8%	Pred. No. 7.9e+03		
Matches 21	Conservative 0	Mismatches 6	Indels 0	Gaps 0
Qy	9	ttccacatgagccagcaccacaagt 35		
Db	60	TTCCGACATGAGCAGGAGACTAGT 34		
RESULT 4				
LOCUS	AI158677/c	77 bp	RNA	linear EST 30-SEP-1998
DEFINITION	ucl9ph1.1 f1 scores_mammary_gland.NbMNG Mus musculus cDNA clone IMAGE:1447365 5' similar to gb:M79757 Mouse pyruvate carboxylase homologous protein mRNA, 3 (MOUSE);, mRNA sequence.			
ACCESSION	AI158677			
VERSION	AI158677.1			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	Mammalia: Eutheria; Rodentia; Sciuromorphi: Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 77) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The Mashu-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project Mashu-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:920681 Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1..77 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_image="1447365" /clone_lib="Soares_mammary_gland_NbMWG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT7T3D-Pac (pharmacia ) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' TGTATCCAAATCTGAAGTGGAGCGCGCGCAATGCTTTTCTTTTCTTTTCTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Palmita Bonaldo."
BASE COUNT	17 a 15 c 29 g 16 t
ORIGIN	
Query Match	48.3%; Score 17.4; DB 9; Length 77;
Best Local Similarity	77.8%; Pred. No. 8.1e+03;
Matches	21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	9 ttccacatgagccagacaccaaagt 35                         DB 48 TGCTTCATGAGCGAAGTCACACAGT 22
RESULT 5	
LOCUS	A1023530 58 bp mRNA linear EST 27-AUG-1998
DEFINITION	ov97d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643535
LOCUS	3' similar to SW:NIAM_BOVIN_002372 NADH-UBIQUINONE OXIDOREDUCTASE
ASHI SUBUNIT	PRECUSOR ;, mRNA sequence.
ACCESSION	A1023530
VERSION	A1023530.1 GI:3238574
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Euarchyotia:	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia:	Euthera; Primates; Catarrhini; Homiidae; Homo.
NCI-CCAP	htp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute,	Cancer Genome Anatomy Project (CGAP),
TITLE	



BASE COUNT	21 a	22 c	11 g	7 t	1 others
ORIGIN	/clone="016e24" /clone_lib="G" /note="Genoscope sequence ID : COBG016BC12LP1-end : 17"				
Query Match	44.4%	Score 16;	DB 12;	Length 62;	
Best Local Similarity	79.2%	Pred. No. 2.6e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	8	ctccaccatgacgcagacacca 31			
Db	25	CTCACACATGATCTCAGACACCA 48			
RESULT	9				
LOCUS	A2920865	85 bp	DNA	linear	GSS 17-DEC-2001
DEFINITION	1006021F02.2EL_x1 1006 - Rescuemu Grid G zea mays genomic, DNA sequence.				
ACCESSION	A2920865				
VERSION	A2920865.1	GI:13391727			
KEYWORDS	GSS.				
SOURCE	zea mays.				
ORGANISM	zea mays.				
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 85)				
TITLE	Walbot, V.				
JOURNAL	Maize genomic sequences found using engineered Rescuemu transposon Unpublished (2001)				
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1006021 row: 38 Class: transposon-tagged. Location/Qualifiers 1. 85 /organism="Zea mays" /cultivar="mixed background W23/A188/B73" /db_xref="taxon:4577" /clone_lib="1006 - Rescuemu Grid G" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
BASE COUNT	21 a	27 c	27 g	10 t	
ORIGIN					
Query Match	44.4%	Score 16;	DB 12;	Length 85;	
Best Local Similarity	79.2%	Pred. No. 2.9e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

OY 1 gccaaagcttcaccatgagccag 24  
 ||||||| ||| | |||||||  
 Db 59 gccaaagcaccagccagccag 82

RESULT 10  
 AA062074/c

LOCUS 93 bp mRNA linear EST 23-SEP-1996  
 DEFINITION mJ8f12.r1 Soares mouse p3MNF19.5 Mus musculus cDNA clone  
 IMAGE:482735 5' similar to gb:219054 BETA-CATENIN (HUMAN);  
 gb:M90364 Mouse (MOUSE);, mRNA sequence.

ACCESSION AA062074  
 VERSION AA062074.1 GI:1555873  
 KEYWORDS EST.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 93)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE The WashU-HMT Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMT Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LINL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:293479

Trace considered overall poor quality  
 Seg primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 1.

FEATURES  
 Source location/Qualifiers

1..93  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:482735"  
 /clone\_lib="Soares mouse p3MNF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: pT7T3D (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer. 15',  
 TGTTCACATCTGAGTGGAGCGCGCATTTTCTTTTCTTTTCTTTT 3',  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Patima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 13 a 15 c 41 g 24 t  
 ORIGIN

Query Match 44.4%; Score 16; DB 9; Length 93;  
 Best Local Similarity 79.2%; Pred. No. 2.9e+04;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 9 ttccacatgagccagcaccacaa 32  
 | ||||| ||| ||| |||||  
 Eb 93 ttccacatgagcaccacaccaa 70

RESULT 11  
 A2499552/c

LOCUS A2499552 71 bp DNA linear GSS 05-OCT-2000  
 DEFINITION IM0337H19F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
 clone U06C1M0337H19 F, DNA sequence.  
 ACCESSION A2499552  
 VERSION A2499552.1 GI:10678493  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 71)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0337 row: H column: 19  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends

High quality sequence stop: 71.

FEATURES  
 Source location/Qualifiers

1..71  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U06C1M0337H19"  
 /clone\_lib="Mouse 10kb plasmid U06C1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/anases/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (911473211419b1AF129072.1), a copy-number  
 inducible derivative of plasmid RI. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 16 a 15 c 17 g 23 t  
 ORIGIN

Query Match 43.9%; Score 15.8; DB 12; Length 71;  
 Best Local Similarity 74.1%; Pred. No. 3.2e+04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 8 ctccacatgagccagcaccacaa 34  
 ||||||| ||| ||| |||||  
 Db 69 ctccacatgagcaccacacaa 43

RESULT 12

R46756/c 80 bp mRNA linear EST 10-MAY-1995  
LOCUS yj54b02.s1 Soares breast 2NBHST Homo sapiens CDNA clone  
IMAGE:152523 3', mRNA sequence.  
ACCESSION R46756  
VERSION R46756.1 GI:806153  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 811  
High quality sequence stops: 59 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 811 Std Error: 0.00  
Seq primer: Promega -21m13  
High quality sequence stop: 59.  
Location/Qualifiers  
1..80  
/organism="Homo sapiens"  
/db\_xref="GDB:564740"  
/db\_xref="taxon:9606"  
/clone="IMAGE:152523"  
/clone\_lib="Soares breast 2NBHST"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: breast; Vector: pRT73D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGAGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 21 a 24 c 15 g 19 t 1 others  
ORIGIN

Query Match 43.9%; Score 15.8; DB 10; Length 80;  
Best Local Similarity 74.1%; Pred. No. 3.3e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 7 gcttcacatgagcagacaccaa 33  
||||| ||||||| ||||| ||  
Db 44 gcttctacacatgacagacacattaa 18

RESULT 13  
B1197684 43 bp mRNA linear EST 10-JUL-2001  
LOCUS B1197684  
DEFINITION 602757596f1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:4893191 5',  
RNA sequence.  
ACCESSION B1197684  
VERSION B1197684.1 GI:14652704  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 43)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L1CM1774 row: p column: 24  
High quality sequence stop: 43.  
Location/Qualifiers  
1..43  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4893191"  
/clone\_lib="NIH\_MGC\_19"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pOT87; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 6 a 12 c 15 g 10 t  
ORIGIN

Query Match 43.3%; Score 15.6; DB 10; Length 43;  
Best Local Similarity 70.0%; Pred. No. 3.2e+04;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 3 gaaagcttcacatgagcagacaccaa 32  
||||| ||||||| ||||| ||  
Db 37 GAACGGCTCTCTCAGATCCGTAGACCAA 8

RESULT 14  
BF311795 43 bp mRNA linear EST 21-NOV-2000  
LOCUS BF311795  
DEFINITION 601897304f1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:4126512 5',  
RNA sequence.  
ACCESSION BF311795  
VERSION BF311795.1 GI:11259557  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 43)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L1CM1016 row: h column: 01  
High quality sequence stop: 43.  
Location/Qualifiers

source

1. .43  
/organism="Homo sapiens"  
/db xref="taxon:9606"  
/clone="IMAGE:4126512"  
/clone\_lib="NIH\_MGC\_19"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT  
ORIGIN  
6 a 12 c 15 g 10 t

Query Match  
Best Local Similarity 70.0%; Score 15.6; DB 10; Length 43;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

2y 3 gaaagcttcacccatgagccagacaccaa 32  
||| | ||| ||| ||| | ||| |||  
db 37 GAACGGCTCTCCAGGATCCCGTAGACCAA 8

RESULT 15  
3P312493/C 43 bp mRNA linear EST 21-NOV-2000  
LOCUS 601897453F1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:4126932 5',  
DEFINITION mRNA sequence.  
ACCESSION BF312493  
VERSION BF312493.1 GI:11260305  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
1 (bases 1 to 43)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov  
Plate: L1CM1017 row: 1 column: 13  
High quality sequence stop: 43.  
Location/Qualifiers

## FEATURES

source

1. .43  
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/db xref="taxon:9606"  
/clone="IMAGE:4126932"  
/clone\_lib="NIH\_MGC\_19"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT  
ORIGIN

6 a 12 c 15 g 10 t

Query Match  
Best Local Similarity 70.0%; Score 15.6; DB 10; Length 43;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 3 gaaagcttcacccatgagccagacaccaa 32  
||| | ||| ||| ||| | ||| |||  
Db 37 GAACGGCTCTCCAGGATCCCGTAGACCAA 8

Search completed: June 22, 2002, 04:59:26  
Job time: 3226 sec

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